

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: June 20, 2005, 19:55:54 ; Search time 29.4726 Seconds
(without alignments)
1123.030 Million cell updates/sec
Title: US-10-734-126-3
Perfect score: 1809
Sequence: 1 MAQKENSYPWPYGRQTAPSG.....PWVRANSRRVLPSPALQSV 344
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 7
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 49%
Maximum Match 100%
Listing first 65000 summaries
Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1507.5	83.3	345	JC4665	protein kinase (EC
2	1069	59.1	395	JCS975	aurora-related kin
3	1062	58.7	389	S52242	protein kinase (EC
4	1050.5	58.1	403	JCS974	aurora-related kin
5	1050.5	58.1	407	S52243	p46Sg265 protein -
6	940	52.0	294	T10690	serine/threonine-s
7	921.5	50.9	282	H84653	probable protein k

ALIGNMENTS

Query Match 59.1%; Score 1069; DB 2; Length 395;
Best Local Similarity 61.4%; Pred. No. 2.2e-39;
Matches 210; Conservative 42; Mismatches 70; Indels 20; Gaps 5;
QY 14 RQTAPSGSLTPQVRVLR----KEPVTSPALVLS-----RSNVQPTAAPGQKVM 58
DB 45 RVLCPNSQRFVSQAQKLGAGQKPAKPKQLPAASVPRPVSRLLNPNQNEPAASGNDSEK 104
QY 59 ENSS--GTPDILTRHTTIDDFIGRPLGKGFNGVYLAREKKSHFIVALKVLPKQIEKE 116
DB 105 EQASLQKTEDTKKROWTLEDFIGRPLGKGFNGVYLAREKSKFTLALKVLPKQIEKE 164
QY 117 GVEHQLRREIEIOAHLHPNIRLNYFYDRIIRYILLEYAPRGELYKELOKSCCTDEOR 176
DB 165 NVEHQURREVEIQSHLRHPNIRLRYFYFDATRVILLEYAPRGELYKELOKSCCTDEOR 224

Query Match 59.1%; Score 1069; DB 2; Length 395;
Best Local Similarity 61.4%; Pred. No. 2.2e-39;
Matches 210; Conservative 42; Mismatches 70; Indels 20; Gaps 5;
QY 14 RQTAPSGSLTPQVRVLR----KEPVTSPALVLS-----RSNVQPTAAPGQKVM 58
DB 45 RVLCPNSQRFVSQAQKLGAGQKPAKPKQLPAASVPRPVSRLLNPNQNEPAASGNDSEK 104
QY 59 ENSS--GTPDILTRHTTIDDFIGRPLGKGFNGVYLAREKKSHFIVALKVLPKQIEKE 116
DB 105 EQASLQKTEDTKKROWTLEDFIGRPLGKGFNGVYLAREKSKFTLALKVLPKQIEKE 164
QY 117 GVEHQLRREIEIOAHLHPNIRLNYFYDRIIRYILLEYAPRGELYKELOKSCCTDEOR 176
DB 165 NVEHQURREVEIQSHLRHPNIRLRYFYFDATRVILLEYAPRGELYKELOKSCCTDEOR 224

Query Match 59.1%; Score 1069; DB 2; Length 395;
Best Local Similarity 61.4%; Pred. No. 2.2e-39;
Matches 210; Conservative 42; Mismatches 70; Indels 20; Gaps 5;
QY 14 RQTAPSGSLTPQVRVLR----KEPVTSPALVLS-----RSNVQPTAAPGQKVM 58
DB 45 RVLCPNSQRFVSQAQKLGAGQKPAKPKQLPAASVPRPVSRLLNPNQNEPAASGNDSEK 104
QY 59 ENSS--GTPDILTRHTTIDDFIGRPLGKGFNGVYLAREKKSHFIVALKVLPKQIEKE 116
DB 105 EQASLQKTEDTKKROWTLEDFIGRPLGKGFNGVYLAREKSKFTLALKVLPKQIEKE 164
QY 117 GVEHQLRREIEIOAHLHPNIRLNYFYDRIIRYILLEYAPRGELYKELOKSCCTDEOR 176
DB 165 NVEHQURREVEIQSHLRHPNIRLRYFYFDATRVILLEYAPRGELYKELOKSCCTDEOR 224

F;146-154/Region: protein kinase ATP-binding motif

Query Match 58.1%; Score 1050.5; DB 2; Length 407;
Best Local Similarity 56.3%; Pred. No. 1.4e-38;
Matches 205; Conservative 46; Mismatches 71; Indels 42; Gaps 4;

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QY 11 PYGROTAPSGSLTLPORVLRKEPVTSPALVMSR---SNVQPT-----AAPGQKME- 59
DB 32 POSTQRPFGTAVSAQRILGFSNVPORVLAQAQKPIILSSQKPTQIPLRPATQGHOSK 91
QY 60 -----NSSGTPDI-----LTRHFTDIDDFEIGRPLGKGF 88
DB 92 QGFENENPQOTSHSTPNVEKKGSTDOGKTSAPVKEGKKQWCLDFEIGRPLGKGF 151
QY 89 GNVYLAREKSHFIVALKVLFKSOIEKEGVEHOLRREIEIOAHLHPNLRNLRLNYFYD 148
DB 152 GNVYLARESKETILALKVLFKQLEKAGVHQRLREVEIQSHLRHPNLRNLRLNYGYF 211
QY 149 RIVLILEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHGKVIHRDIKPN 208
DB 212 RVYLILDYAPGGELFRELQKCTFDDORSAMYIKQALAEALLYCHSKKVIHRDIKPN 271
QY 209 GLKGLKLIADFGWSVHAPSRLRRRTMCTGLDYLPPMEIEGRMHNEKVDLWCIGVLCY 268
DB 272 GSNGLKLIADFGWSVHAPSRLRTLCGLDYLPPMEIEGRMHDETVDLMSLGLVLCY 331
QY 269 GNPFPSSASHNETYRIRIVKVDLKFPPASVPTGAQDLISKLRHNPSERLPLAQVSA 328
DB 332 GKPFETDTHQETYYRIRISKVEFYQPVVSEARDLVSKLKHNPNRHLPLKGVLEHP 391
QY 329 ANSR 332
DB 392 KNSQ 395
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RESULT 6

T10690 serine/threonine-specific protein kinase homolog T16118.40 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004C;Accession: T10690
R;Revan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro

submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16533

A;Accession: T10690

A;Molecule type: DNA

A;Residues: 1-294 <BEV>

A;Cross-references: UNIPROT:Q9M077; EMBL:AL049915; GSPDB:GN00062; ATSP:T16118.40

A;Experimental source: cultivar Columbia; BAC clone T16118

C;Genetics:

A;Gene: ATSP:T16118.40

A;Map position: 4

A;Introns: 12/3; 52/3; 101/3; 133/3; 165/3; 198/1; 237/2; 261/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

F;29-282/Domain: protein kinase homology <KIN>

Query Match 52.0%; Score 940; DB 2; Length 294;
Best Local Similarity 60.3%; Pred. No. 5.5e-34;
Matches 179; Conservative 47; Mismatches 63; Indels 8; Gaps 4;

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QY 49 PTAPQKQWENSSGTPDILTRHFTDIDDFEIGRPLGKGFNVLAREKSHFIVALKVL 108
DB 4 PTETQOE-KEASASAAAAQKWTLSDFDIGNPLGRKFGHVLAREKRSNHHVALKVL 62
QY 109 FKSOIEKEGVEHOLRREIEIOAHLHPNLRNLRLNYFYDRLRRIYLLILEYAPRGELYKELQK 168
DB 63 FKSQLQSQSQVEHOLRREVEIQSHLRHPNLRNLRLNYGYDQKRVYLLILEYAAARGELYKDLQK 122
QY 169 SCTFFDQRTATIMEELADALMYCHGKVIHRDIKPNLMLGLKGLKLIADFGWSVHAPS 228
DB 123 CKYFSERRAATYVASLARALYCHGKVIHRDIKPNLMLGLKGLKLIADFGWSVHTFN- 181
QY 229 RRTMCGTLDYLPPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFPSSASHNETYRIRIVK 288
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DB 182 RRTMCGTLDYLPPEMVESEVHDASVDIWSGLLCYEFYLVGVPFFEMESDYYRRLVQV 241
QY 289 DLKFPAS--VPTGAQDLISKLRHNPSERLPLAQVSAHPWVRANSRRVLPSPASQV 343
DB 242 DLKFPKPIISASAKDLISQMLVKESSQRLPLHKLLEHPWIVQNA----DPSGIYRV 294
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RESULT 7

H84653

probable protein kinase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84653

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84653

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-282 <STO>

A;Cross-references: UNIPROT:O82309; GB:AE002093; NID:g3643610; PIDN:AAC42257.1; GSPDB:GN

C;Genetics:

A;Gene: At2g25880

A;Map position: 2

C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 50.9%; Score 921.5; DB 2; Length 282;
Best Local Similarity 63.7%; Pred. No. 3.3e-33;
Matches 174; Conservative 42; Mismatches 50; Indels 7; Gaps 3;

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QY 70 RHFTDIDDFEIGRPLGKGFNVLAREKSHFIVALKVLFKSOIEKEGVEHOLRREIEIQ 129
DB 12 KRWTSDFDIGNPLGRKFGHVLAREKSDHIVALKVLFKQQLQSQSQVEHQLRREVEIQ 71
QY 130 AHLHPNLRNLRLNYFYDRLRRIYLLILEYAPRGELYKELQKSCTFDEQRTATIMEELADALM 189
DB 72 SHLRHPNLRNLRLNYGYFYDQKRVYLLILEYAVRGELYKELQKCYFSERRAATYVASLARALI 131
QY 190 YCHGKVIHRDIKPNLMLGLKGLKLIADFGWSVHAPSRLRRTMCGTLDYLPPEMIEGRM 249
DB 132 YCHGKVIHRDIKPNLMLGLKGLKLIADFGWSVHTFN-RRRTMCGTLDYLPPEMVESE 190
QY 250 HNEKVDLWCIGVLCYELLVGNPPFPSSASHNETYRIRIVKVDLKEPAS--VPTGAQDLISKL 307
DB 191 HDASVDIWSGLLCYEFYLVGVPFFEMESDYYRRLVQVLDLKEPKPIVSSAKDLISQM 250
QY 308 LRHPNPSERLPLAQVSAHPWVRANSRRVLPSPASL 340
DB 251 LVKESQRLALHKLLEHPWIVQNA----DPSGL 279
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Search completed: June 20, 2005, 20:07:57

Job time : 32.4726 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:59:50 ; Search time 44.2383 Seconds
(without alignments)
680.035 Million cell updates/sec

Title: US-10-734-126-4
Perfect score: 2110
Sequence: 1 MDRSKENCISGPVKATAPVG.....TANSSKPSNCKNESASKQS 403

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%
Maximum Match 100%
Listing first 65000 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2110	100.0	403	2	US-08-755-728-4
2	2110	100.0	403	2	US-08-974-655-4
3	2110	100.0	403	3	US-09-283-011-4
4	2110	100.0	403	4	US-09-012-135A-4
5	2110	100.0	488	4	US-09-949-016-10461
6	2110	100.0	488	4	US-09-949-016-10462
7	1058	50.1	363	4	US-09-949-016-9826
8	1057.5	50.1	344	2	US-08-755-728-3
9	1057.5	50.1	344	2	US-08-974-655-3
10	1057.5	50.1	344	3	US-09-283-011-3
11	1057.5	50.1	344	4	US-09-012-135A-3
12	1050	49.8	343	4	US-09-485-534-4
13	1046	49.6	347	2	US-09-016-000-1

ALIGNMENTS

RESULT 1
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-755-728-4

Query Match 100.0%; Score 2110; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-179;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRPVPLQ 60
DB 1 MDRSKENCISGPVKATAPVGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRPVPLQ 60
QY 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSKOPLPSAPENNPEELASKQKN 120
DB 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSKOPLPSAPENNPEELASKQKN 120
QY 121 ESKKQKQWALEDFEIGRPLGKGFKNVYLAREKQSFILALKVLFKAQLEKAGVEHQJLR 180
DB 121 ESKKQKQWALEDFEIGRPLGKGFKNVYLAREKQSFILALKVLFKAQLEKAGVEHQJLR 180
QY 181 EYEQSHLRHPNLLRLYGFHDATRVYLILEYAPLGTVTYRELQKLSKDFQRTATYTTEL 240
DB 181 EYEQSHLRHPNLLRLYGFHDATRVYLILEYAPLGTVTYRELQKLSKDFQRTATYTTEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTLLCGTLDYLPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTLLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCLYEFVLVGPFPPEANTYQETIKRISRVFTFPDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGLVCLYEFVLVGPFPPEANTYQETIKRISRVFTFPDFVTEGARDLI 360
QY 361 SLLKKNPSQRPMLREVLEHPWITANSSKPSNCKNESASKQS 403
DB 361 SLLKKNPSQRPMLREVLEHPWITANSSKPSNCKNESASKQS 403

Db 361 SLLKHNPSQRPMLREVLEHPWITANSSKPSNCKNESASKOS 403

RESULT 2

US-08-974-655-4
; Sequence 4, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-974-655-4

Query Match 100.0%; Score 2110; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-179;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRSKNCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRPVPLQ 60
Db 1 MDRSKNCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRPVPLQ 60
QY 61 AQKLVSHKPVQKQKQLOATSVPHVPSPLNNTQSKQPLPSAPENNPEELASKQKN 120
Db 61 AQKLVSHKPVQKQKQLOATSVPHVPSPLNNTQSKQPLPSAPENNPEELASKQKN 120
QY 121 EESKQKQWALEDFEIGRLPGKGFNGVYLAREKOSKFIILAKVLFKAQLEKAGVEHQLRR 180
Db 121 EESKQKQWALEDFEIGRLPGKGFNGVYLAREKOSKFIILAKVLFKAQLEKAGVEHQLRR 180

QY 181 EVEIQSHLHPNLRILRYGYFHDATRVYLLILEVAPLGTVTVRELQKLSKPFDEQRTATYITEL 240
Db 181 EVEIQSHLHPNLRILRYGYFHDATRVYLLILEVAPLGTVTVRELQKLSKPFDEQRTATYITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGMSVHAPSSRRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGMSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCLCYEFLVKGKPPPEANTYQETYKRIISRVETFFDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGLVCLCYEFLVKGKPPPEANTYQETYKRIISRVETFFDFVTEGARDLI 360
QY 361 SLLKHNPSQRPMLREVLEHPWITANSSKPSNCKNESASKOS 403
Db 361 SLLKHNPSQRPMLREVLEHPWITANSSKPSNCKNESASKOS 403

RESULT 3

US-09-283-011-4
; Sequence 4, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: NO
; ANTI-SENSE: NO
US-09-283-011-4


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Query Match      100.0%; Score 2110; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 60
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Db 86 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 145
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   |||||
Db 146 AQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 205
   |||||
QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKOSKFILALKVLFKAQLEKAGVEHQLR 180
   |||||
Db 206 EESKKQWALEDFEIGRPLGKGFNGVYLAREKOSKFILALKVLFKAQLEKAGVEHQLR 265
   |||||
QY 181 EVEIOSHLRHPNIRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKDFEQTATYITEL 240
   |||||
Db 266 EVEIOSHLRHPNIRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKDFEQTATYITEL 325
   |||||
QY 241 ANALSYCHSKRVTHRIDIKPENLLSGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
   |||||
Db 326 ANALSYCHSKRVTHRIDIKPENLLSGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 385
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QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRISRVEFTFPDFVTEGARDLI 360
   |||||
Db 386 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRISRVEFTFPDFVTEGARDLI 445
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QY 361 SLLKHNPQSOPRMLREVLEHPWITANSSKPSNCKNESASKOS 403
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Db 446 SLLKHNPQSOPRMLREVLEHPWITANSSKPSNCKNESASKOS 488
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RESULT 6
US-09-949-016-10462
; Sequence 10462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10462
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10462

Query Match      100.0%; Score 2110; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 60
   |||||
Db 86 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 145
   |||||
QY 61 AQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 120
   |||||
Db 146 AQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 205
   |||||
QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKOSKFILALKVLFKAQLEKAGVEHQLR 180
   |||||

Query Match      100.0%; Score 1058; DB 4; Length 363;
Best Local Similarity 59.2%; Pred. No. 6e-86;
Matches 218; Conservative 43; Mismatches 83; Indels 24; Gaps 6;

QY 43 QAQRVCLPSSNSQRPVLOAQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKQPL 102
   ::|||
Db 3 ESSLALDPSSPPPPFSLRMAQKENSYPWYGRQTAPSGSLT-LPQVLR-----KEPV 53
   |||||
QY 103 -PSA-----PENNPPEELASKOKNESKK-----RQWALEDFEIGRPLGKGFNGVYL 150
   |||||
Db 54 TFSALVMSRSNVQPTAAPFCQKMENSSGTPDILTRHFTDIDFEIGRPLGKGFNGVYL 113
   |||||
QY 151 REKOSKFILALKVLFKAQLEKAGVEHQLRREVEIOSHLRHPNIRLRYGYFHDATRVYLIL 210
   |||||
Db 114 REKSHFIVALKVLFKASQIEKEGVEHQLRREVEIOSHLRHPNIRLRYGYFHDATRVYLIL 173
   |||||
QY 211 EVAPLGTVYRELOKLSKDFEQTATYITELANALSYCHSKRVTHRIDIKPENLLSGAGEL 270
   |||||
Db 174 EVAPRGELYKELQKSCFTDFEQTATIMEELADALMYCHGKVKVTHRIDIKPENLLGLKGE 233
   |||||
QY 271 KIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPE 330
   |||||
Db 234 KIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPE 293
   |||||
QY 331 ANTYQETKYKRISRVEFTFPDFVTEGARDLISLLKHNPQSOPRMLREVLEHPWITANSSK- 389
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QY 390 --PSNCQN 395
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Query Match      100.0%; Score 2110; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 60
   |||||
Db 86 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLO 145
   |||||
QY 61 AQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 120
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Db 146 AQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 205
   |||||
QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKOSKFILALKVLFKAQLEKAGVEHQLR 180
   |||||

Query Match      100.0%; Score 1058; DB 4; Length 363;
Best Local Similarity 59.2%; Pred. No. 6e-86;
Matches 218; Conservative 43; Mismatches 83; Indels 24; Gaps 6;

QY 43 QAQRVCLPSSNSQRPVLOAQKLVSSHKPVQKOKQOLQATSVPHPSRPLNNTOKSKQPL 102
   ::|||
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   |||||
QY 103 -PSA-----PENNPPEELASKOKNESKK-----RQWALEDFEIGRPLGKGFNGVYL 150
   |||||
Db 54 TFSALVMSRSNVQPTAAPFCQKMENSSGTPDILTRHFTDIDFEIGRPLGKGFNGVYL 113
   |||||
QY 151 REKOSKFILALKVLFKAQLEKAGVEHQLRREVEIOSHLRHPNIRLRYGYFHDATRVYLIL 210
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Db 114 REKSHFIVALKVLFKASQIEKEGVEHQLRREVEIOSHLRHPNIRLRYGYFHDATRVYLIL 173
   |||||
QY 211 EVAPLGTVYRELOKLSKDFEQTATYITELANALSYCHSKRVTHRIDIKPENLLSGAGEL 270
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Db 174 EVAPRGELYKELQKSCFTDFEQTATIMEELADALMYCHGKVKVTHRIDIKPENLLGLKGE 233
   |||||
QY 271 KIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPE 330
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Db 234 KIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPE 293
   |||||
QY 331 ANTYQETKYKRISRVEFTFPDFVTEGARDLISLLKHNPQSOPRMLREVLEHPWITANSSK- 389
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Db 294 SASHNETYTRIVKVDLKFFPASVPTGAQDLISKLLRNPSERLPLAQVSAHPWTRANSRRV 353
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QY 390 --PSNCQN 395
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Db 354 LPPSALQS 361
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RESULT 8
US-08-755-728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-755-728-3

Query Match 50.1%; Score 1057.5; DB 2; Length 344;
Best Local Similarity 63.2%; Pred. No. 6.2e-86;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPRPLNNTQSKQPL-PSA-----PENNPEELASKQKNVESKK-----RQWA 129
Db 22 STLQFVLR-----KEFVTPSALVMSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY 130 LEDPEIGRPLGKGFNVYLAREKQKFIILAKVLPKAOLEKAGVHOLRREVEIQSHLR 189
Db 74 IDDFEIGRPLGKGFNVYLAREKKGHFIVALKVLPKQKIEKGVSHQRLRREIEIOAHLH 133
QY 190 HPNIRLYGYFHDATRVYLILEYAPLGTVYVRELQKLSKFDQRTATVITELANALSYCHS 249
Db 134 HPNIRLYNYFYDRRIYLLILEYAPRGELYKELQKCTFDQRTATIMEELADALMYCHG 193
QY 250 KRVIHRDIPENLLGKAGELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMNEK 309
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Db 194 KKVTHRDIPENLLGKAGELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMNEK 253
QY 310 VDLWSLGLVLCYEFVLGVKPPPEANTYQETKYKRISRVETFPDFVTEGARDLIYSLKKHNP 369
Db 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIYKVDLKFPASVPTGAQDLISKLLRNPS 313
QY 370 QRPMLREVLEHPWITANSSK---PSNCQN 395
Db 314 ERLPLAQVSAHPWVRANSRRLVLPSPALQS 342
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RESULT 9
US-08-974-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-974-655-3

Query Match 50.1%; Score 1057.5; DB 2; Length 344;
Best Local Similarity 63.2%; Pred. No. 6.2e-86;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPRPLNNTQSKQPL-PSA-----PENNPEELASKQKNVESKK-----RQWA 129
Db 22 STLQFVLR-----KEFVTPSALVMSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
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;
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-012-135A-3

Query Match 50.1%; Score 1057.5; DB 4; Length 344;
Best Local Similarity 63.2%; Pred. No. 6.2e-86;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSPVPSVPLNNTQKSKPL-PSA-----PENNPEELASKQKNESSK-----ROWA 129
DB 22 STLPRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHQRLRRREVEIOSHLR 189
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QY 250 KRVIHDKIPENLLSAGELKIADFGWSVHAPSSRRRTTCGTLDPPEMIEGRMHDEK 309
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QY 310 VDWLSGLVLCYBFLGKPPPEANTYQETKYRISRVETFPDFVTEGARDLISRLKKNPS 369
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RESULT 12
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; Sequence 4, Application US/09485534
; Patent No. 6759212
; GENERAL INFORMATION:
; APPLICANT: TATSUKA, MASAAKI
; APPLICANT: TERADA, YASUHIKO
; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS
; FILE REFERENCE: 050499/0102
; CURRENT APPLICATION NUMBER: US/09/485,534
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/JP98/03641
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 233371/1997
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-485-534-4

Query Match 49.8%; Score 1050; DB 4; Length 343;
Best Local Similarity 57.6%; Pred. No. 2.9e-85;
Matches 204; Conservative 51; Mismatches 73; Indels 26; Gaps 4;
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QY 156 KFILALKVLFKAQLEKAGVEHQRLRRREVEIOSHLRHPNILLRLYGFHDATVYLILEYAPL 215
DB 103 RFIVALKILFKSQIEKEGVEHQRLRRREIEIOAHLKHPNILLQLYNYFYDQQRILYLEVAPR 162

QY 216 GTVYRELQKLSKDEQRTATYITELANALSYCHSKSVIHRDIKPENLLSAGELKIADF 275
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QY 276 GWSVHAPSSRRRTTCGTLDPPEMIEGRMHDEKVDLWSLGLVLCYBFLGKPPPEANTYQ 335
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QY 336 EYKYSRISRVETFPDFVTEGARDLISRLKKNPSQRPMLREVLEHPWITANSK 389
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RESULT 13
US-09-016-000-1
; Sequence 1, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,000
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
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; LIBRARY: HMC1NOT01
; CLONE: 2940
US-09-016-000-1

Query Match      49.6%; Score 1046; DB 2; Length 347;
Best Local Similarity 62.7%; Pred. NO. 6.e-85;
Matches 208; Conservative 41; Mismatches 57; Indels 26; Gaps 6;

QY 82 TSVPHVSRPLNNTQSKQPL-PSA-----PENNPEELASKOKNEESKK-----ROWA 129
Db 22 STLPRVLR-----KEPVTPSALVLMRSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKLVLFKAQLEKAGVEHQHQRREVEIQSHLR 189
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Db 134 HNNILRLYNYFYDRRRYIYILEYAPRGELYKELOKSCTFEQRTATVRAIMEELADALMY 193

QY 247 CHSKRVITHRDIKPENLLIGSAGELKIADFGWSVHAPSSRRRTTCGTLDYLPPEMIEGRMH 306
Db 194 CHGKRVITHRDIKPENLLIGLKGELKIADFGWSVHAPSLRRKTCMCGTLDYLPPEMIEGRMH 253

QY 307 DEKVDLMSLGVLCYEFVLGKPPFEANTYQETKYKRISRVEFTFPDFVTEGARDLISRLLKH 366
Db 254 NEKVDLMLCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPTGAQDLISKLLRH 313

QY 367 NPSQRPLREVLEHPWITANSK---PSNCQN 395
Db 314 NPSERLPLAQVSAHPWVRANSRRVLPPLPSALQS 345
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Job time : 47.2383 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2005, 19:47:43 ; Search time 77.6867 Seconds
(without alignments)

1991.894 Million cell updates/sec

Title: US-10-734-126-4

Perfect score: 2110

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Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 49%

Maximum Match 100%

Listing first 65000 summaries

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Published Applications_AA.*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2110	100.0	403	11	US-09-784-332-4
3	2110	100.0	403	15	US-10-087-684-47
4	2110	100.0	403	15	US-10-218-779-47
5	2110	100.0	403	16	US-10-734-126-4
6	2110	100.0	420	15	US-10-264-049-3090
7	2109	100.0	403	14	US-10-060-065-12
8	2109	100.0	403	14	US-10-059-585-33
9	2109	100.0	403	15	US-10-087-684-48
10	2109	100.0	403	15	US-10-218-779-48
11	2104	99.7	403	15	US-10-295-027-1206

Sequence 49, Appl	15	US-10-087-684-49	403	99.7	2104
Sequence 49, Appl	15	US-10-218-779-49	403	99.7	2104
Sequence 35, Appl	403	US-10-188-832-35	403	99.7	2104
Sequence 65, Appl	403	US-10-751-736-65	403	99.7	2104
Sequence 187, Appl	403	US-10-781-581-187	403	99.7	2104
Sequence 2, Appl	403	US-10-209-324-2	403	99.7	2103
Sequence 7, Appl	403	US-10-028-021-7	403	99.3	2095
Sequence 50, Appl	403	US-10-087-684-50	403	99.3	2095
Sequence 50, Appl	403	US-10-218-779-50	403	99.3	2095
Sequence 51, Appl	402	US-10-087-684-51	402	91.7	1935.5
Sequence 14, Appl	402	US-10-218-779-51	402	91.7	1935.5
Sequence 14, Appl	403	US-10-087-684-14	403	91.2	1924
Sequence 125, Appl	403	US-10-218-779-14	403	91.2	1924
Sequence 3, Appl	322	US-10-664-421-125	322	80.1	1690
Sequence 3, Appl	344	US-09-012-135A-3	344	50.1	1057.5
Sequence 13, Appl	344	US-09-784-332-3	344	50.1	1057.5
Sequence 34, Appl	344	US-10-060-065-13	344	50.1	1057.5
Sequence 214, Appl	344	US-10-059-585-34	344	50.1	1057.5
Sequence 203, Appl	344	US-10-171-311-214	344	50.1	1057.5
Sequence 101, Appl	344	US-10-295-027-203	344	50.1	1057.5
Sequence 93, Appl	344	US-10-173-999-101	344	50.1	1057.5
Sequence 3, Appl	344	US-10-188-832-93	344	50.1	1057.5
Sequence 4, Appl	344	US-10-734-126-3	344	50.1	1057.5
Sequence 136, Appl	343	US-10-429-849-4	343	49.8	1050
Sequence 98, Appl	347	US-09-974-298-136	347	49.6	1046
	320	US-10-403-571-98	320	49.5	1045

ALIGNMENTS

RESULT 1

US-09-012-135A-4
; Sequence 4, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-012-135A-4

Query Match 100.0%; Score 2110; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.2e-147;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLTQFPQCNPLPVNSGOAQRVLCPSSNQRPVPLQ 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLTQFPQCNPLPVNSGOAQRVLCPSSNQRPVPLQ 60
QY 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENNPEBELASKQKN 120
Db 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENNPEBELASKQKN 120
QY 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
Db 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL 240
Db 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCEYELVGGKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGLVCEYELVGGKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
QY 361 SRLLKHNPSQRPMLREVLEHPMTITANSKPSNCKNESASKQS 403
Db 361 SRLLKHNPSQRPMLREVLEHPMTITANSKPSNCKNESASKQS 403

RESULT 2
US-09-784-332-4
; Sequence 4, Application US/09784332
; Publication No. US2005002938A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,332
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; FILING DATE: 16-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/283,011
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: November 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-784-332-4

Query Match 100.0%; Score 2110; DB 11; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.2e-147;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLTQFPQCNPLPVNSGOAQRVLCPSSNQRPVPLQ 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLTQFPQCNPLPVNSGOAQRVLCPSSNQRPVPLQ 60
QY 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENNPEBELASKQKN 120
Db 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENNPEBELASKQKN 120
QY 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
Db 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL 240
Db 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCEYELVGGKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGLVCEYELVGGKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
QY 361 SRLLKHNPSQRPMLREVLEHPMTITANSKPSNCKNESASKQS 403
Db 361 SRLLKHNPSQRPMLREVLEHPMTITANSKPSNCKNESASKQS 403

RESULT 3
US-10-087-684-47
; Sequence 47, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
```

APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David J.
APPLICANT: Grosse, William M.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie, J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Shenoy, Suresh G.
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.M.
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Gangolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCES: 21402-214 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 47
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-087-684-47

Query Match 100.0%; Score 2110; DB 15; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.2e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60

QY 61 AQKLVSSHFPVQKQKQLOQATSVPHVPSRPLNNTOKSQPLPSAPENNPPEELASKQKN 120
Db 61 AQKLVSSHFPVQKQKQLOQATSVPHVPSRPLNNTOKSQPLPSAPENNPPEELASKQKN 120

QY 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180
Db 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180

QY 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240
Db 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240

QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSHAPSSRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSHAPSSRTTLCGTLDYLPPEM 300

QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYRISVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYRISVEFTFPDFVTEGARDLI 360

QY 361 SRLLKKNPQRPMLREVLEHPWITANSSKPSNQNCKESASKQS 403
Db 361 SRLLKKNPQRPMLREVLEHPWITANSSKPSNQNCKESASKQS 403

RESULT 4
US-10-218-779-47
Sequence 47, Application US/10218779
Publication No. US20040029222A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William
APPLICANT: Alsbrook II, John
APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-779-47

Query Match 100.0%; Score 2110; DB 15; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.2e-147; Mismatches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60

QY 61 AQKLVSSHFPVQKQKQLOQATSVPHVPSRPLNNTOKSQPLPSAPENNPPEELASKQKN 120
Db 61 AQKLVSSHFPVQKQKQLOQATSVPHVPSRPLNNTOKSQPLPSAPENNPPEELASKQKN 120

QY 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180

Db 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALVKLFAQLEKAGVEHQLRR 180
Qy 181 EYEIOHSLRHPNLRILRGYFHDATRVYLILEVAPLGTVYRELOKLSKDFEORTATYITEL 240
Db 181 EYEIOHSLRHPNLRILRGYFHDATRVYLILEVAPLGTVYRELOKLSKDFEORTATYITEL 240
Qy 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPPM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPPM 300
Qy 301 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYKRI SRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYKRI SRVEFTFPDFVTEGARDLI 360
Qy 361 SRLLNKHPNPSQRPMLREVLEHHPMTANSSKPSNCKNESASKOS 403
Db 361 SRLLNKHPNPSQRPMLREVLEHHPMTANSSKPSNCKNESASKOS 403

RESULT 5

US-10-734-126-4
; Sequence 4, Application US/10734126
; Publication No. US20040265852A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; Moseie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,126
; FILING DATE: 15-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,332
; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 09/283,011
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: November 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-734-126-4
Query Match 100.0%; Score 2110; DB 16; Length 403;
Best Local Similarity 100.0%; Pred. No. 3.2e-147;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDRSKENCISGPKVATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
Db 1 MDRSKENCISGPKVATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
Qy 61 AOKLVSSHKPVQNKQKQLOATSVPHVSRPLNNTQKSKQPLSPENNPPEELASKQKN 120
Db 61 AOKLVSSHKPVQNKQKQLOATSVPHVSRPLNNTQKSKQPLSPENNPPEELASKQKN 120
Qy 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALVKLFAQLEKAGVEHQLRR 180
Db 121 ESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALVKLFAQLEKAGVEHQLRR 180
Qy 181 EYEIOHSLRHPNLRILRGYFHDATRVYLILEVAPLGTVYRELOKLSKDFEORTATYITEL 240
Db 181 EYEIOHSLRHPNLRILRGYFHDATRVYLILEVAPLGTVYRELOKLSKDFEORTATYITEL 240
Qy 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPPM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPPM 300
Qy 301 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYKRI SRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYKRI SRVEFTFPDFVTEGARDLI 360
Qy 361 SRLLNKHPNPSQRPMLREVLEHHPMTANSSKPSNCKNESASKOS 403
Db 361 SRLLNKHPNPSQRPMLREVLEHHPMTANSSKPSNCKNESASKOS 403

RESULT 6

US-10-264-049-3090
; Sequence 3090, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3090
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3090

Query Match 100.0%; Score 2110; DB 15; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.4e-147;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDRSKENCISGPKVATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
Db 18 MDRSKENCISGPKVATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 77
Qy 61 AOKLVSSHKPVQNKQKQLOATSVPHVSRPLNNTQKSKQPLSPENNPPEELASKQKN 120

Db	78	AQLVSSHKPVONQKQKQLOQATSVPHPSVRPLNNTQKSKQPLSPAPENNPESELASKQKN	137
Qy	121	EESKRGWALEDFEIGRPLGKGFQNVYLAREKQSKFIALAKVLKPALEKAGVEHQLR	180
Db	138	EESKRGWALEDFEIGRPLGKGFQNVYLAREKQSKFIALAKVLKPALEKAGVEHQLR	197
Qy	181	EVEIQSHLRHFNILRLGYGFHDATRVYLILEVAPLGTVTVYRELQKLSKDFEORTATYITEL	240
Db	198	EVEIQSHLRHFNILRLGYGFHDATRVYLILEVAPLGTVTVYRELQKLSKDFEORTATYITEL	257
Qy	241	ANALSYCHSKRVIHRDIKPNLLGSGAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM	300
Db	258	ANALSYCHSKRVIHRDIKPNLLGSGAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM	317
Qy	301	IEGRMHKEVDLWSLGSVLCYEFVLGKPPPEANTYQETYKRISRVEFTPPDFVTEGARDLI	360
Db	318	IEGRMHKEVDLWSLGSVLCYEFVLGKPPPEANTYQETYKRISRVEFTPPDFVTEGARDLI	377
Qy	361	SRLLKHPNSQBPMLREVLHPWITANSKPSNCKNESASKOS	403
Db	378	SRLLKHPNSQBPMLREVLHPWITANSKPSNCKNESASKOS	420

RESULT 7

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US-10-060-065-12
; Sequence 12, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-095002
; CURRENT APPLICATION NUMBER: US/10/060,065
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-065-12

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1	MDRSKENCISG	PVKATAPVG	GPKEVLVTQ	QFP	CQNP	LPVNSG	QAORVLC	PSNSSOR	PIQP	60				
61	AQKLVSSH	KPVONKOKO	LOQATSV	PHVPS	RPLNNT	QKSQ	PLPSAP	ENNP	PEELAS	KQKN	120			
61	AQKLVSSH	KPVONKOKO	LOQATSV	PHVPS	RPLNNT	QKSQ	PLPSAP	ENNP	PEELAS	KQKN	120			
121	EESKKRQW	ALED	DFEIGR	PLGK	GFNV	LARE	KOSK	FTLAL	KVLP	KAQLEKAG	VEHQLR	180		
121	EESKKRQW	ALED	DFEIGR	PLGK	GFNV	LARE	KOSK	FTLAL	KVLP	KAQLEKAG	VEHQLR	180		
181	EVEIQSHLR	HPNII	RLXYG	FHDAT	RVYLIL	EYAP	PLGT	VYVRE	LQKLSK	DFEQRTAT	YITEL	240		
181	EVEIQSHLR	HPNII	RLXYG	FHDAT	RVYLIL	EYAP	PLGT	VYVRE	LQKLSK	DFEQRTAT	YITEL	240		
241	ANALYSCH	SKRV	IHRD	IKPEN	LLG	SAGEL	KIAD	FGW	SHAP	SSRRTT	LCGTL	DYLP	300	
241	ANALYSCH	SKRV	IHRD	IKPEN	LLG	SAGEL	KIAD	FGW	SHAP	SSRRTT	LCGTL	DYLP	300	
301	IEGRMHDE	KVDL	WSLG	VLCY	EFLV	GKPP	PEANTY	QET	YKRI	SRVE	FTPDF	VTEG	ARDLI	360
301	IEGRMHDE	KVDL	WSLG	VLCY	EFLV	GKPP	PEANTY	QET	YKRI	SRVE	FTPDF	VTEG	ARDLI	360
361	SRLLKHN	PSQRP	MLRE	VLEHP	WITANS	KPN	CNKES	SAS	KOS	403				
361	SRLLKHN	PSQRP	MLRE	VLEHP	WITANS	KPN	CNKES	SAS	KOS	403				

RESULT 8

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US-10-059-585-33
; Sequence 33, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-33

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Best Local Similarity 99.8%; Pred. No. 3.8e-147;
Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRPVLO 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRPVLO 60
QY 61 AOKLVSSHKPVQKQKQLOQATSVPHVPSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
Db 61 AOKLVSSHKPVQKQKQLOQATSVPHVPSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
QY 121 ESKKRQWALEDEIFGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
Db 121 ESKKRQWALEDEIFGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIOSHLRHPNLRLLGYGFHDATRVYLLILEVAPLGTVYRELOKLSKDFEORTATVITEL 240
Db 181 EVEIOSHLRHPNLRLLGYGFHDATRVYLLILEVAPLGTVYRELOKLSKDFEORTATVITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRISRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRISRVEFTFPDFVTEGARDLI 360
QY 361 SRLKHNPQSOPMLREVLEHPWITANSSKPSNCKNESASKOS 403
Db 361 SRLKHNPQSOPMLREVLEHPWITANSSKPSNCKNESASKOS 403
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RESULT 9

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US-10-087-684-48
; Sequence 48, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
```

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; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 48
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-48

Query Match 100.0%; Score 2109; DB 15; Length 403;
Best Local Similarity 99.8%; Pred. No. 3.8e-147;
Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRPVLO 60
Db 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRPVLO 60
QY 61 AOKLVSSHKPVQKQKQLOQATSVPHVPSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
Db 61 AOKLVSSHKPVQKQKQLOQATSVPHVPSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
QY 121 ESKKRQWALEDEIFGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
Db 121 ESKKRQWALEDEIFGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIOSHLRHPNLRLLGYGFHDATRVYLLILEVAPLGTVYRELOKLSKDFEORTATVITEL 240
Db 181 EVEIOSHLRHPNLRLLGYGFHDATRVYLLILEVAPLGTVYRELOKLSKDFEORTATVITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRISRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRISRVEFTFPDFVTEGARDLI 360
QY 361 SRLKHNPQSOPMLREVLEHPWITANSSKPSNCKNESASKOS 403
Db 361 SRLKHNPQSOPMLREVLEHPWITANSSKPSNCKNESASKOS 403
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RESULT 10

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US-10-218-779-48
; Sequence 48, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
```

```
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Baha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-48

Query Match      100.0%; Score 2109; DB is; Length 403;
Best Local Similarity 99.8%; Pred. No. 3.8e-147;
Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCFNSSSQRIPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCFNSSSQRIPLQ 60
QY 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSPQPLSPAPENNPEELASKQKN 120
DB 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSPQPLSPAPENNPEELASKQKN 120
QY 121 BESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRR 180
DB 121 BESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNTRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATYITEL 240
DB 181 EVEIQSHLRHPNTRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATYITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDTLPPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDTLPPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRSRVEFTFPDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRSRVEFTFPDFVTEGARDLI 360
QY 361 SRLLKHNPSPQRMLEVLHPMTITANSKPSNCKNESASQK 403
DB 361 SRLLKHNPSPQRMLEVLHPMTITANSKPSNCKNESASQK 403

RESULT 11
US-10-295-027-1206
; Sequence 1206, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1206
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1206

Query Match      99.7%; Score 2104; DB 15; Length 403;
Best Local Similarity 99.8%; Pred. No. 8.9e-147;
Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCFNSSSQRIPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCFNSSSQRIPLQ 60
QY 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSPQPLSPAPENNPEELASKQKN 120
DB 61 AOKLVSSHKPVQKQKQLOQATSVPHVSRPLNNTOKSPQPLSPAPENNPEELASKQKN 120
QY 121 BESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRR 180
DB 121 BESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNTRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATYITEL 240
DB 181 EVEIQSHLRHPNTRLRYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATYITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDTLPPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDTLPPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRSRVEFTFPDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKRSRVEFTFPDFVTEGARDLI 360
QY 361 SRLLKHNPSPQRMLEVLHPMTITANSKPSNCKNESASQK 403
DB 361 SRLLKHNPSPQRMLEVLHPMTITANSKPSNCKNESASQK 403

RESULT 12
US-10-087-684-49
; Sequence 49, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
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; PRIOR FILING DATE: 2001-07-27
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (31)..(31)
 ; OTHER INFORMATION: Xaa is Ile or Phe
 US-10-209-324-2

 Query Match 99.7%; Score 2103; DB 14; Length 403;
 Best Local Similarity 99.8%; Pred.No. 1.1e-146;
 Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 MDRSKENCISGPVKATAPVGGPKRVILVTQFPQCNPLPVNSGQAQRVLCPSNSSQRVPLQ 60
 Db 1 MDRSKENCISGPVKATAPVGGPKRVILVTQFPQCNPLPVNSGQAQRVLCPSNSSQRVPLQ 60

 Qy 61 AQLKVVSHKPVQNKOKQLQATSVHPVSRPLNNTOKSQPLPSAPENNPEELASKQKN 120
 Db 61 AQLKVVSHKPVQNKOKQLQATSVHPVSRPLNNTOKSQPLPSAPENNPEELASKQKN 120

 Qy 121 EESKKEQWALEDFEIGRPLGKGGFNVYLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180
 Db 121 EESKKEQWALEDFEIGRPLGKGGFNVYLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180

 Qy 181 EVIQSHLRHNPILRLYGFDHATRVYLILEYAPLGTIVVRELQKSKFDEQRTATYITEL 240
 Db 181 EVIQSHLRHNPILRLYGFDHATRVYLILEYAPLGTIVVRELQKSKFDEQRTATYITEL 240

 Qy 241 ANALSVCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAPSSRRTTLCGLDYLPPEM 300
 Db 241 ANALSVCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAPSSRRTTLCGLDYLPPEM 300

 Qy 301 IEGRMHDEKVDLMSLGVLCVEFLVGGKPPPEANTYQETIKRISRVEFTFPDFVTEGARDLI 360
 Db 301 IEGRMHDEKVDLMSLGVLCVEFLVGGKPPPEANTYQETIKRISRVEFTFPDFVTEGARDLI 360

 Qy 361 SRLLLKKNPSQRPMLREVLEHPWITANSSKPSNCONKESASKQS 403
 Db 361 SRLLLKKNPSQRPMLREVLEHPWITANSSKPSNCONKESASKQS 403

 RESULT 18
 US-10-026-021-7
 ; Sequence 7, Application US/10026021
 ; Publication No. US20030027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-001210US
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human ARK mitotic kinase
 US-10-026-021-7

 Query Match 99.3%; Score 2095; DB 14; Length 403;

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; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curasequest version 0.1
; SEQ ID NO 50
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-50

Query Match          99.3%; Score 2095; DB 15; Length 403;
Best Local Similarity 99.3%; Pred. No. 4.le-146;
Matches 400; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  1 MDRSKENCISGPVKATAPVCGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSSQRVPLQ 60
    |||
Db  1 MDRSKENCISGPVKATAPVCGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSSQRVPLQ 60
    |||

Qy  61 AQLVSSHKVPQNKQKQLQATSVPHVPVSPLNNTQSKOPLPSAPENNPEEELASKQKN 120
    |||
Db  61 AQLVSSHKVPQNKQKQLQATSVPHVPVSPLNNTQSKOPLPSAPENNPEEELASKQKN 120
    |||

Qy  121 EESKCRQWALEDFEIGRPLGKGFNGVYLAREKOSKFI LAKVL FKAQLEKAGVEHQLR 180
    |||
Db  121 EESKCRQWALEDFEIGRPLGKGFNGVYLAREKOSKGI LAKVL FKAQLEKAGVEHQLR 180
    |||

Qy  181 EVIQSHLRHPNLRILGYGPHDATRVYLIILEYAPLGTVYRELOKLSKFDQRTATYITEL 240
    |||
Db  181 EVIQSHLRHPNLRILGYGPHDATRVYLIILEYAPLGTVYRELOKLSKFDQRTATYITEL 240
    |||

Qy  241 ANALSYCHSKRVHRDIKPNELLGSGAGELKLIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
    |||
Db  241 ANALSYCHSKRVHRDIKPNELLGSGAGELKLIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
    |||

Qy  301 IEGRMHDEKVDLMSLGLVCYEFVLGKPPFPFANTYQETYKRSIRVEFTFPDFVTEGARDLI 360
    |||
Db  301 IEGRMHDEKVDLMSLGLVCYEFVLGKPPFPFANTYQETYKRSIRVEFTFPDFVTEGARDLI 360
    |||

Qy  361 SRLLLKHNPSQRPMLREVLEHPWITANSSKPSNCONKESASKQS 403
    |||
Db  361 SRLLLKHNPSQRPMLREVLEHPWITANSSKPSNCONKESASKQS 403
    |||

RESULT 20
US-10-218-779-50
; Sequence 50, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytak, Kimberly
; APPLICANT: Baldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Veizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan

```

Qy	241	ANALSYCHSKRVTHRIDIKPENLLLSGAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM	300
Db	241	ANALSYCHSKRVTHRIDIKPENLLLSGAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM	300
Qy	301	IEGRMHDEKVDLWSLGLVCYEFVLGKPPPPFPAANTYQETIKRISRVFEFFDPFVTEGARDLI	360
Db	301	IEGRMHDEKVDLWSLGLVCYEFVLGKPPPPFPAANTYQETIKRISRVFEFFDPFVTEGARDLI	360
Qy	361	SRLLLKHNPSPQRMRLREVLEHPWITANSKPSNQNKNESASKQS	403
Db	361	SRLLLKHNPSPQRMRLREVLEHPWITANSKPSNQNKNESASKQS	403

RESULT 20

US-10-218-779-50

Sequence 50, Application US/10218779

Publication No. US20040029222A1

GENERAL INFORMATION:

APPLICANT: Edinger, Shlomit

APPLICANT: MacDougall, John

APPLICANT: Millet, Isabelle

APPLICANT: Ellerman, Karen

APPLICANT: Stone, David

APPLICANT: Gerlach, Valerie

APPLICANT: Grosse, William

APPLICANT: Alsobrook II, John

APPLICANT: Lepley, Denise

APPLICANT: Rieger, Daniel

APPLICANT: Burgess, Catherine

APPLICANT: Casman, Stacie

APPLICANT: Spytek, Kimberly

APPLICANT: Boldog, Ferenc

APPLICANT: Li, Li

APPLICANT: Padigaru, Muralidhara

APPLICANT: Mishra, Vishnu

APPLICANT: Patturajan, Meera

APPLICANT: Shenoy, Suresh

APPLICANT: Rastelli, Luca

APPLICANT: Tchernev, Veizhar

APPLICANT: Vernet, Corine

APPLICANT: Zerhusen, Bryan

Qy	61	AQKLVSSHYPVQNKQKQLOATSVPHVPSRPLNNTQKSKQPLSPAPENNPEELASKQKN	120
Db	61	AQKLVSSHYPVQNKQKQLOATSVPHPASRPLNNTQSKQSPLSAPENNPEELASKQKN	120
Qy	121	EESKKGQWALEDFEIGRPLGKGFQGVYLAREKQSKFTIALKVLUFKAQLKAGVEHQLR	180
Db	121	EESKKGQWALEDFEIGRPPCKGFQGVYLAREKQSKFTILRVLUFKAQLKAGVEHQLR	180
Qy	181	EVEIQSHLRHPNIRLYGYFHDATRVYILLEYAPLGTVYRELOKLSKFDQRTATVITEL	240
Db	181	EVEIQSHLQHPNIRLYGYFHDATRVYILLEYTLETVNTLELOKLSKFDQRTATVITEL	240
Qy	241	ANALSYSCHSKRVTHRDIKPENLLIGSAGELKIAFGVSHAPSSRRITLCGTLDYLPPEM	300
Db	241	ASALSYSCHSKRVTHRDIKPENLLIGSAGELIANFGVSEHAPSSRRITLCGTLDYLPPEM	300
Qy	301	IEGRMHDEKVDLWSLGVLCYEELVGKPPFEANTYQETVKRISRVEFTFPDVFVEGARDLI	360
Db	301	IEGRMHDEKVDLWSLGVLCCEELVGKPPFEANTYQETVKRISRVEFTFPDVFVEGARDLI	360
Qy	361	SRLLKKNPSQRPMLEVLHPWITANSKPSNCKNGSASKQS	403
Db	361	SRLLKHPVQRPMLEVLHPWITANSKPSNCKNGESTSKYS	403

```

RESULT 24
US-10-218-779-14
; Sequence 14, Application US/10218779
; Publication No. US2004002922A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millett, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zethusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nu
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/2
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,83
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-9
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,18
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,65
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,45
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216

```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-14

Query Match          91.2%; Score 1924; DB 15; Length 403;
Best Local Similarity 91.8%; Pred. No. 1.6e-133;
Matches 370; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy      1  MDRSKENCISGPVKATAPVGPKRVLVTQPPCONPLPVNSGOAQRVLCPSNSSQRVPLQ 60
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1  MDGSENCISGPVEAKTPVGPERHLVTQPPCONPLPANSGQAQWVLCPSNSSQRVPLQ 60
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      61  AQKLVSSEKVEQKQKQLQATSVPHPVSRPLNNTQSKQPLPSAPENNPEEELASKOKN 120
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61  AQKLVSSEKVPQKQKQLQATSVPHPASRPLNNTQNSKQSPLSAPENNPEEELASKOKN 120
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      121  EESKKRQWALEDEFGRLPGKGFNGVYLAREQSKFILAALKVLFKAQLEKAGVEHOLRR 180
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121  EESKKRQWALEDELEGRPGKGFNGVYLAREQSKFILAALRVLFKAQLEKAGVEHOLRR 180
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      181  EVETQSHLRHPNTRLRLGYGFHDATRVYLIILEYAPLGTVYRELOKLSKFDEORTATYITEL 240
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181  EVEIQSHLQPNTRLRLGYGFHDATRVYLIILEYTPLETVNTELOKLSKFDEORTATYITEL 240
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      241  ANALSYCHSKRVRIHRDIKPENLLLGSGAGELKIADFGWSVHAPSSRRRTLCTGLDYLPPEM 300
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      241  ASALSYCHSKTVRIHRDIKPENLLLLGSGAGELEIANFGWSEHAPSSRRRTLCTGLDYLPPEM 300
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      301  IEGRMHDEKVDLWSLGLVCFYELVGKPPPPANTYQETYKELSRVEFTFPDFVTEGARDLI 360
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      301  IEGRMHDEKVDLWSLGLVCLCFYELVGKPPPPANTYQETYKELSRVEFTFPDFVTEGARDLI 360
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      361  SRLLLKHNPQSOPMLREVLEHPWITANSKSPKSNCKESASKQS 403
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      361  SRLLLKHVPQSOPMLREVLEFPWITANSKSPKSNCKESTSKYS 403
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 25
US-10-664-421-125
; Sequence 125, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRAHVA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 125
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-125

```

```

Query Match      80.18; Score 1690; DB 16; Length 322;
Best Local Similarity 100.0%; Pred. NO. 2.2e-116;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      82  TSPHPVSRPLNNTQSKQPLPAPENNPPEELASKQNEESKCKQWALDEFEIGRPLGK 141
      |||
Db      1  TSPHPVSRPLNNTQSKQPLPAPENNPPEELASKQNEESKCKQWALDEFEIGRPLGK 60

```

QY 142 GKGNVYLAREKSKFILALKVLFKAQLEKAGVEHQHRLREVEIQSHLRHNIILRYGYFH 201
DB 61 GKGNVYLAREKSKFILALKVLFKAQLEKAGVEHQHRLREVEIQSHLRHNIILRYGYFH 120
QY 202 DATRVVILLYAYPLGTVYRELQKSKFDEORTATYITELANALSYCHSKRVIHRDIKPN 261
DB 121 DATRVVILLYAYPLGTVYRELQKSKFDEORTATYITELANALSYCHSKRVIHRDIKPN 180
QY 262 LLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGLCYE 321
DB 181 LLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEKVDLWSLGLCYE 240
QY 322 FLVCKPPPEANTYQETKYRISRVETFPDPFVTEGARDLISRLIKHNPSQRPMLREVLEHP 381
DB 241 FLVCKPPPEANTYQETKYRISRVETFPDPFVTEGARDLISRLIKHNPSQRPMLREVLEHP 300
QY 382 WITANSKSPNSCONKESASKQS 403
DB 301 WITANSKSPNSCONKESASKQS 322

RESULT 26

US-09-012-135A-3
; Sequence 3, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-012-135A-3

Query Match 50.1%; Score 1057.5; DB 9; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRLNNTQSKQPL-PSA-----PENNPEELASQKNBESKK-----ROWA 129
DB 22 STLQORVLR-----KEPVTPSALVLMRSRNVQPTAAPGQKWMENSSGTPDILTRHFT 73
QY 130 LEDFEIRPLGKGFNGVYLAREKSKFILALKVLFKAQLEKAGVEHQHRLREVEIQSHLR 189
DB 74 IDDFEIRPLGKGFNGVYLAREKSKSHFVALKVLKFSQIEKEGVEHQHRLREVEIQSHLR 133
QY 190 HNNILRYGVFFHDATRVVILLYAYPLGTVYRELQKSKFDEORTATYITELANALSYCHS 249
DB 134 HNNILRYGVFFHDATRVVILLYAYPLGTVYRELQKSKFDEORTATYITELANALSYCHS 193
QY 250 KRVIHREDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 309
DB 194 KRVIHREDIKPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 253
QY 310 VDLWSLGLCYEFLVCKPPPEANTYQETKYRISRVETFPDPFVTEGARDLISRLIKHNPS 369
DB 254 VDLWSLGLCYEFLVCKPPPEANTYQETKYRISRVETFPDPFVTEGARDLISRLIKHNPS 313
QY 370 QRPMLREVLEHPWITANSK---PSNCON 395
DB 314 QRPMLREVLEHPWITANSK---PSNCON 342

RESULT 27

US-09-784-332-3
; Sequence 3, Application US/09784332
; Publication No. US20050002938A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,332
; FILING DATE: 16-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/283,011
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: November 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995


```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Watburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 231/282
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1800
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 344 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-784-332-3

Query Match      50.1%; Score 1057.5; DB 11; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRLNNTQSKQPL-PSA-----PENNPEELASKQKNBESKK-----RQWA 129
Db 22 STLQQRVLR-----KEVTPSALVLMRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRLPGKGFNVYLAREKSKFILAUKVLKFAOLEKAGVHQLRREVEIQSHLR 189
Db 74 IDDFEIGRLPGKGFNVYLAREKSKSHFIVALKVLFKSQIEKEGVHQLRREIEIQAHLLH 133
QY 190 HPNILLRGYFHDATRVYLILEVAPLGTVYVRELOKLSKFDDEORTATVITELANALSYCHS 249
Db 134 HPNILLRYNYFYDRRIYLLILEVAPRGELYKELQKSCCTDEQRTATIMBELADALMYCHG 193
QY 250 KRVIHRDIKPENLLGSGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 309
Db 194 KKVHRDIKPENLLGKGLKELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMNEK 253
QY 310 VDLWSLGVLCYFLVGKPPFEANTYQTYKRISRVEFTFPDFVTEGARDLISRLLKHNPS 369
Db 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPFPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHPWITANSKK---PSNCON 395
Db 314 ERLPLAQVSAHPWVRANSRRVLPPSALQS 342
```

```
RESULT 28
US-10-060-065-13
/ Sequence 13, Application US/10060065
/ Publication No. US20030017480A1
/ GENERAL INFORMATION:
/ APPLICANT: Toshio Ota
/ APPLICANT: Takao Isogai
/ APPLICANT: Tetsuo Nishikawa
/ APPLICANT: Koji Hayashi
/ APPLICANT: Kaoru Otsuka
/ APPLICANT: Jun-Ichi Yamamoto
/ APPLICANT: Shizuko Ishii
/ APPLICANT: Tomoyasu Sugiyama
/ APPLICANT: Ai Wakamatsu
/ APPLICANT: Keiichi Nagai
/ APPLICANT: Tetsuji Otsuki
/ APPLICANT: Shin-Ichi Funahashi
/ APPLICANT: Chiaki Senoo
/ APPLICANT: Jun-Ichi Nezu
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
/ FILE REFERENCE: 06501-099002
/ CURRENT APPLICATION NUMBER: US/10/060, 065
/ CURRENT FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP00/05061
```

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/ PRIOR FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: US 60/159,590
/ PRIOR FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US 60/183,322
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: JP 11-248036
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: JP 2000-118776
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: JP 2000-183767
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: JP 2000-241899
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 13
/ LENGTH: 344
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-060-065-13

Query Match      50.1%; Score 1057.5; DB 14; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRLNNTQSKQPL-PSA-----PENNPEELASKQKNBESKK-----RQWA 129
Db 22 STLQQRVLR-----KEVTPSALVLMRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRLPGKGFNVYLAREKSKFILAUKVLKFAOLEKAGVHQLRREVEIQSHLR 189
Db 74 IDDFEIGRLPGKGFNVYLAREKSKSHFIVALKVLFKSQIEKEGVHQLRREIEIQAHLLH 133
QY 190 HPNILLRGYFHDATRVYLILEVAPLGTVYVRELOKLSKFDDEORTATVITELANALSYCHS 249
Db 134 HPNILLRYNYFYDRRIYLLILEVAPRGELYKELQKSCCTDEQRTATIMBELADALMYCHG 193
QY 250 KRVIHRDIKPENLLGSGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 309
Db 194 KKVHRDIKPENLLGKGLKELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMNEK 253
QY 310 VDLWSLGVLCYFLVGKPPFEANTYQTYKRISRVEFTFPDFVTEGARDLISRLLKHNPS 369
Db 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPFPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHPWITANSKK---PSNCON 395
Db 314 ERLPLAQVSAHPWVRANSRRVLPPSALQS 342
```

```
RESULT 29
US-10-059-585-34
/ Sequence 34, Application US/10059585
/ Publication No. US20030082776A1
/ GENERAL INFORMATION:
/ APPLICANT: Ota, Toshio
/ APPLICANT: Isogai, Takao
/ APPLICANT: Nishikawa, Tetsuo
/ APPLICANT: Hayashi, Koji
/ APPLICANT: Otsuka, Kaoru
/ APPLICANT: Yamamoto, Jun-ichi
/ APPLICANT: Ishii, Shizuko
/ APPLICANT: Sugiyama, Tomoyasu
/ APPLICANT: Wakamatsu, Ai
/ APPLICANT: Nagai, Keiichi
/ APPLICANT: Otsuki, Tetsuji
/ APPLICANT: Funahashi, Shin-Ichi
/ APPLICANT: Senoo, Chiaki
/ APPLICANT: Nezu, Jun-Ichi
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
/ TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
/ FILE REFERENCE: 06501-098001
/ CURRENT APPLICATION NUMBER: US/10/059,585
```



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; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-34

Query Match      50.1%; Score 1057.5; DB 14; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRPLNNTQSKQPL-PSA-----PENNPEELASQKNVESKK-----RQWA 129
Db 22 STLQQRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKWMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNVYLAREKQSKFIALKVLKPAQLEKAGVEHOLRREVEIQSHLR 189
Db 74 IDDFEIGRPLGKGFNVYLAREKSKSHFIVALKVLFKQIEKEGVEHOLRREIEIQAHLLH 133

QY 190 HPNILRLYGVFHDATRVYLILEVAPLGTVVRELOKLSKDEQRTATVITELANALSYCHS 249
Db 134 HPNILRLYNYFYDRRIYLLILEVAPRGELYKELQKSCTFDEQRTATIMEELADALMYCHG 193

QY 250 KRVIHRIKPENLILLGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 309
Db 194 KKVIHRIKPENLILLGKGLKELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253

QY 310 VDLWSGLVLCYELFVGKPPPEANTYQETRYKISRVEFTFPDFVTEGARDLISLLKHNP 369
Db 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPASVPTGAQDLISKLLRHNP 313

QY 370 QRPMLREVLHPMTANSSK---PSNCON 395
Db 314 ERPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 30
US-10-171-311-214
; Sequence 214, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10171.311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-214

Query Match      50.1%; Score 1057.5; DB 14; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRPLNNTQSKQPL-PSA-----PENNPEELASQKNVESKK-----RQWA 129
Db 22 STLQQRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKWMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNVYLAREKQSKFIALKVLKPAQLEKAGVEHOLRREVEIQSHLR 189
Db 74 IDDFEIGRPLGKGFNVYLAREKSKSHFIVALKVLFKQIEKEGVEHOLRREIEIQAHLLH 133

QY 190 HPNILRLYGVFHDATRVYLILEVAPLGTVVRELOKLSKDEQRTATVITELANALSYCHS 249
Db 134 HPNILRLYNYFYDRRIYLLILEVAPRGELYKELQKSCTFDEQRTATIMEELADALMYCHG 193

QY 250 KRVIHRIKPENLILLGAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMHDEK 309
Db 194 KKVIHRIKPENLILLGKGLKELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253

QY 310 VDLWSGLVLCYELFVGKPPPEANTYQETRYKISRVEFTFPDFVTEGARDLISLLKHNP 369
Db 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPASVPTGAQDLISKLLRHNP 313

QY 370 QRPMLREVLHPMTANSSK---PSNCON 395
Db 314 ERPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 31
US-10-295-027-203
; Sequence 203, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natacha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
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; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-203

Query Match      50.1%; Score 1057.5; DB 15; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKOKNEESKK-----ROWA 129
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QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKVLKFAOLEKAGVHQRRVEIQSHLR 189
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QY 190 HENILRLYGFHDATRVYLLILEYAPLGTVYRELOKLSKFEDEORTATYITELANALSYCHS 249
Db 134 HENILRLYNYFYDRRIYVLLIYAPRGELYKELQKSCFDEORTATIMEELADALMYCHG 193

QY 250 KRVIHRIKPENLILGSGAGELKIADFGWSVHAPSSRRRTTCGTLDYLPPEMIEGRMHDEK 309
Db 194 KRVIHRIKPENLILGSGAGELKIADFGWSVHAPSSRRRTTCGTLDYLPPEMIEGRMHDEK 253

QY 310 VDLWSLGVLCYFELVKGKPPFEANTYQETVKRISRVFEFTPPDFVTGARDLISRLLKHNP 369
Db 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIRVKVDLFPASVPTGAQDLISKLRLHNP 313

QY 370 QRPMLREVLEHPWITANSK---PSNCON 395
Db 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
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RESULT 32
US-10-173-999-101
; Sequence 101, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-101
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Query Match      50.1%; Score 1057.5; DB 15; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKOKNEESKK-----ROWA 129
Db 22 STLQVRLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKVLKFAOLEKAGVHQRRVEIQSHLR 189
Db 74 IDDFEIGRPLGKGFNGVYLAREKSKSHFIALKVLKFAOLEKAGVHQRRVEIQSHLR 133

QY 190 HENILRLYGFHDATRVYLLILEYAPLGTVYRELOKLSKFEDEORTATYITELANALSYCHS 249
Db 134 HENILRLYNYFYDRRIYVLLIYAPRGELYKELQKSCFDEORTATIMEELADALMYCHG 193

QY 250 KRVIHRIKPENLILGSGAGELKIADFGWSVHAPSSRRRTTCGTLDYLPPEMIEGRMHDEK 309
Db 194 KRVIHRIKPENLILGSGAGELKIADFGWSVHAPSSRRRTTCGTLDYLPPEMIEGRMHDEK 253

QY 310 VDLWSLGVLCYFELVKGKPPFEANTYQETVKRISRVFEFTPPDFVTGARDLISRLLKHNP 369
Db 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIRVKVDLFPASVPTGAQDLISKLRLHNP 313

QY 370 QRPMLREVLEHPWITANSK---PSNCON 395
Db 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
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US-10-188-832-93
; Sequence 93, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-93

Query Match      50.1%; Score 1057.5; DB 15; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKOKNEESKK-----ROWA 129
Db 22 STLQVRLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKVLKFAOLEKAGVHQRRVEIQSHLR 189
Db 74 IDDFEIGRPLGKGFNGVYLAREKSKSHFIALKVLKFAOLEKAGVHQRRVEIQSHLR 133
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QY 190 HNNILRLGYGPHDATRVYLILEYAPLGTVYRLOKLSKDEQRTATYITELANALSYCHS 249
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DB 194 KKVHRDIKPNLLGSGAGELKIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 253
QY 310 VDLWSGLVLCYEFVGVKPPPEANTYQTYKRIISRVFTFPDFVTEGARDLISRLKHNPS 369
DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHWPITANSK---PSNCQN 395
DB 314 ERLPLAQVSAHPWVRANSRRVLPPLSALQS 342

RESULT 34
US-10-734-126-3
; Sequence 3, Application US/10734126
; Publication No. US20040265852A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: 533 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/734,126
FILING DATE: 15-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/784,332
FILING DATE: 16-Feb-2001
APPLICATION NUMBER: 09/283,011
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: November 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-734-126-3
Query Match 50.1%; Score 1057.5; DB 16; Length 344;
Best Local Similarity 63.2%; Pred. No. 9.9e-70;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 82 TSVPHFVSRLPNNLTOKSKQPL-PSA-----PENNPEELASQKQNESSKK-----RQWA 129
DB 22 STLPRQVLR-----KEPTVPSALVMSRNVQPTAAPGQKVMENSGSTPDILTTHFT 73
QY 130 LEDFEIGRPLGKGFNGVYLAREKOSKFILAKLVFKAOLEKAGVEHQHQRREVEIOSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKKSHTFVALKLVFKSQIEKEGVEHQHQRREVEIOAHILH 133
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DB 134 HNNILRLYNYFYDRRIYILILEYAPRGELYKSLQKSCTFDEQRTATIMEELADALMYCHG 193
QY 250 KRVIHRDIKPNLLGSGAGELKIADFGWSVHAPSSRRRTLCGTLDYLPPEMIEGRMHDEK 309
DB 194 KKVHRDIKPNLLGSGAGELKIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 253
QY 310 VDLWSGLVLCYEFVGVKPPPEANTYQTYKRIISRVFTFPDFVTEGARDLISRLKHNPS 369
DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHWPITANSK---PSNCQN 395
DB 314 ERLPLAQVSAHPWVRANSRRVLPPLSALQS 342

RESULT 35
US-10-429-849-4
; Sequence 4, Application US/10429849
; Publication No. US20040029157A1
; GENERAL INFORMATION:
; APPLICANT: TATSUKA, MASAAKI
; APPLICANT: TERADA, YASUHIKO
; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS
; FILE REFERENCE: 050499/0102
; CURRENT APPLICATION NUMBER: US/10/429,849
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US/09/485,534
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/JP98/03641
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 235371/1997
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-429-849-4

Query Match 49.8%; Score 1050; DB 15; Length 343;
Best Local Similarity 57.6%; Pred. No. 3.5e-69;
Matches 204; Conservative 51; Mismatches 73; Indels 26; Gaps 4;
QY 36 PLPVNSGOAQRVLCPSNSSORVPLQAOAKLVSSHKVPQKQKQLOQATSVPHPVSRPLNNT 95
DB 9 PMFYGSKTSQSGL--NTLPQRV-LRKEPAVTPAQALMNR-----SNS 47
QY 96 QKSQPLFSAPEENPEELASQKQNEESKQOWALEDFEIGRPLGKGFNGVYLAREKOS 155
DB 48 QSTAVPGQKLTENKCATALQGSQ-----SRQPTIDNFEIGRPLGKGFNGVYLAREKOS 102
QY 156 KFILAKVLFKAOLEKAGVEHQHQRREVEIQSHLRHPNILRLGYGPHDATRVYLILEYAPL 215

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:57:12 ; Search time 138.649 Seconds
(without alignments)
1488.417 Million cell updates/sec

Title: US-10-734-126-4
Perfect score: 2110
Sequence: 1 MDKSKENCISGPVKATAPVG.....TANSSKPSNCKNESASKOS 403

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%
Maximum Match 100%
Listing first 65000 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2110	100.0	403	1	STK6 HUMAN	014965 homo sapien
2	1686	79.9	397	1	STK6 RAT	P59241 rattus norv
3	1661.5	78.7	386	2	Q8C3H8	Q8C3H8 mus musculu
4	1661	78.7	395	1	STK6 MOUSE	P97477 mus musculu
5	1652	78.3	395	2	Q7TNK2	Q7TNK2 mus musculu
6	1650	78.2	395	2	Q8BP87	Q8BP87 mus musculu
7	1320.5	62.6	408	1	ST6L XENLA	Q91819 xenopus lae
8	1318.5	62.5	408	2	Q6DJK0	Q6DJK0 xenopus lae
9	1295.5	61.4	407	1	STK6 XENLA	Q91820 xenopus lae
10	1204.5	57.1	405	2	Q6DBZ4	Q6DBZ4 brachydanio
11	1071.5	50.8	361	2	Q9DF70	Q9DF70 xenopus lae
12	1071	50.8	320	2	Q6NW76	Q6NW76 brachydanio
13	1069	50.7	368	2	Q6GPL3	Q6GPL3 xenopus lae
14	1067.5	50.6	361	2	Q8JG74	Q8JG74 xenopus lae
15	1067.5	50.6	361	2	Q8D308	Q8D308 xenopus lae
16	1067.5	50.6	371	2	Q7ZYT9	Q7ZYT9 xenopus lae
17	1061	50.3	345	1	AURB MOUSE	Q70126 mus musculu
18	1057.5	50.1	344	1	AURB HUMAN	Q96g4 homo sapien
19	1057	50.1	345	2	Q8C6C1	Q8C6C1 mus musculu
20	1050	49.8	343	1	AURB RAT	Q55099 rattus norv
21	1045	49.5	344	2	Q7YRC6	Q7YRC6 bos taurus

ALIGNMENTS

RESULT 1

STK6_HUMAN

ID STK6_HUMAN STANDARD; PRT; 403 AA.

AC 014965; 060445; 075873; 09BQD6; 09UPG5;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15) (Aurora/IPL1-related kinase 1) (Aurora-related kinase 1) (HARK1) (Aurora-A) (Breast-tumor-amplified kinase).

GN Name=STK6; Synonyms=Aik, ARK1, AURA, BTAK, STK15; Homo sapiens (human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=97298083; PubMed=9153231; DOI=10.1074/jbc.272.21.13766; Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K., Okano Y.;

RA "Cell cycle-dependent expression and spindle pole localization of a novel human protein kinase, Aik, related to Aurora of Drosophila and yeast Ipl1.";

RT J. Biol. Chem. 272:13766-13771(1997).

RL [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250; Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M., Gilbert D.J., Jenkins N.A., Copeland N.G., Yegita H., Okumura K.;

RA "cDNA cloning, expression, subcellular localization, and chromosomal assignment of mammalian aurora homologues, aurora-related kinase (ARK) 1 and 2.";

RT Biochem. Biophys. Res. Commun. 244:285-292(1998).

RL [3]

RN SEQUENCE FROM N.A.

RP TISSUE=Breast;

RX MEDLINE=98442657; PubMed=9771714; DOI=10.1038/2496; Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A., Brinkley B.R., Sen S.;

RA "Tumour amplified kinase STK15/BTAK induces centrosome amplification, aneuploidy and transformation.";

RT Nat. Genet. 20:189-193(1998).

RL [4]

RN SEQUENCE FROM N.A.

RP Wang L., Thibodeau S.;

RA "Mutational analysis of the STK15 gene in human tumors.";

RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.

RL [5]

RN SEQUENCE FROM N.A.

RP MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a; Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp G., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehesvahti M.H., Liversha M.A., Lloyd D.M., Lloyd J.D., Marsh V.L., Martin S.L., McConachie L.J., McIlroy J.C., McKernan A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).

RN [6] SEQUENCE FROM N.A.
 RC TISSUE=Cervix, Colon, Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.S., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP CELL-CYCLE REGULATION.
 RX MEDLINE=21895866; PubMed=11790771; DOI=10.1074/jbc.M108252200;
 RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
 RA Ishigatsubo Y.;
 RT "Cell-cycle-dependent regulation of human aurora A transcription is
 RT mediated by periodic repression of E4TF1.";
 RL J. Biol. Chem. 277:10719-10726 (2002).
 RN [8]
 RP REVIEW.
 RX MEDLINE=211306577; PubMed=11413462; DOI=10.1038/35048096;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32 (2001).
 CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
 CC and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC Maybe involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
 CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 CC colon, ovarian, prostate, neuroblastoma, breast and cervical
 CC cancer cell lines. Expression is cell-cycle regulated, low in
 CC G1/S, accumulates during G2/M, and decreases rapidly after.
 CC -!- PTM: Phosphorylated.
 CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome
 CC aberrations including aneuploidy.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
 CC subfamily.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in positions 105, 125, 129, 235 and 241.
 CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
 CC different proteins, it is clear that they are the same protein.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D84212; BAA33592.1; ALT_FRAME.
 DR EMBL; AF008551; AAC12708.1; -.
 DR EMBL; AF011467; AAC23448.1; -.
 DR EMBL; AF011468; AAC63902.1; -.

DR EMBL; AF195947; AAF29508.1; -.
 DR EMBL; AF195942; AAF29508.1; JOINED.
 DR EMBL; AF195943; AAF29508.1; JOINED.
 DR EMBL; AF195944; AAF29508.1; JOINED.
 DR EMBL; AF195945; AAF29508.1; JOINED.
 DR EMBL; AF195946; AAF29508.1; JOINED.
 DR EMBL; AL121914; CAC12717.1; -.
 DR EMBL; BC001280; AAH01280.1; -.
 DR EMBL; BC002499; AAH02499.1; -.
 DR EMBL; BC006423; AAH06423.1; -.
 DR EMBL; BC027464; AAH27464.1; -.
 DR PDB; 1MQ4; X-ray; A=120-391.
 DR PDB; 1MO4; X-ray; A=107-391.
 DR PDB; 1OL6; X-ray; A=122-403.
 DR PDB; 1OL7; X-ray; A=122-403.
 DR Genew; HGNC:11393; STK15.
 DR Genew; HGNC:11409; STK6.
 DR H-InvDB; HIX0015930; -.
 DR MIM; 602687; -.
 DR MIM; 603072; -.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0005819; C:spindle; TAS.
 DR GO; GO:0004672; F:protein kinase activity; TAS.
 DR GO; GO:0007067; P:mitosis; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW 3D-structure; ATP-binding; Cell cycle; Phosphorylation;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 133 383 Protein kinase.
 FT BIND 139 147 ATP (By similarity).
 FT BINDING 162 162 ATP (By similarity).
 FT ACT_SITE 236 236 Proton acceptor (By similarity).
 FT CONFLICT 31 31 F -> I (in Ref. 3).
 FT CONFLICT 57 57 V -> I (in Ref. 2).
 FT SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;
 SQ
 Query Match 100.0%; Score 2110; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 1.7e-126;
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPKVATAPVGGPKRVLTQQFPCQNPVPVNSGQARVLCPSNSSQRPVPLQ 60

Db 1 MDRSKENCISGPKVATAPVGGPKRVLTQQFPCQNPVPVNSGQARVLCPSNSSQRPVPLQ 60

QY 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQKSKQPLPSAPENNPEELASKQKN 120

Db 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQKSKQPLPSAPENNPEELASKQKN 120

QY 121 ESKKQWALEDFETGRPLGKFGNVYLAREKQSKFIALLKVLFAQLKAGVEHQLRR 180

Db 121 ESKKQWALEDFETGRPLGKFGNVYLAREKQSKFIALLKVLFAQLKAGVEHQLRR 180

QY 181 EYEIQSHLRHPNRLRYGVFHDATRVLLILEVAPLGTVYRELQKLSKDFEQTATVITEL 240

Db 181 EYEIQSHLRHPNRLRYGVFHDATRVLLILEVAPLGTVYRELQKLSKDFEQTATVITEL 240

QY 241 ANALSYCHSKRVIHRIKPEENLLSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPEM 300

Db 241 ANALSYCHSKRVIHRIKPEENLLSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPEM 300

QY 301 IEGRMDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRIISVEFTFPDFVTEGARDLI 360

Db 301 IEGRMDEKVDLWSLGVLCYEFVLGKPPPEANTYQETYKRIISVEFTFPDFVTEGARDLI 360

QY 361 SRLLKHNPSQRMPLREVLHPWITANSSKPSNCKESASKOS 403
 Db 361 SRLLKHNPSQRMPLREVLHPWITANSSKPSNCKESASKOS 403

RESULT 2

STK6 RAT STANDARD; PRT; 397 AA.
 AC P59241;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Aurora-A) (rataAurA).
 GN Name=Stk6; Synonym=Stk15;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar Furth; TISSUE=Mammary gland;
 RX MEDLINE=22119444; PubMed=12124350;
 RA Goepfert T.M., Adigun Y.E., Zhong L., Gay J., Medina D.,
 RA Brinkley W.R.;
 RT "Centrosome amplification and overexpression of aurora A are early
 events in rat mammary carcinogenesis.";
 RL Cancer Res. 62:4115-4122(2002).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21306577; PubMed=11413462; DOI=10.1038/35048096;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
 and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC Maybe involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in mammary gland and tumor.
 CC -!- INDUCTION: Activated by progesterone.
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
 subfamily.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF537333; AA006823.1; -
 CC HSSP; P31751; IGZK.
 CC RGD; 628895; Stk6.
 CC InterPro; IPR011009; Kinase like.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR008271; Ser_thr_pkin_AS.
 CC InterPro; IPR002290; Ser_thr_pkinase.
 CC Pfam; PF00069; Pkinase; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding; Cell cycle; Phosphorylation;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 126 376 Protein kinase.
 FT NP_BIND 132 140 ATP (By similarity).
 FT BINDING 155 155 ATP (By similarity).
 FT

FT ACT SITE 249 249 Proton acceptor (By similarity).
 SQ SEQUENCE 397 AA; 44874 MW; 95DECA2198DCED85 CRC64;
 Query Match 79.9%; Score 1686; DB 1; Length 397;
 Best Local Similarity 83.4%; Pred. No. 1.8e-99;
 Matches 337; Conservative 15; Mismatches 44; Indels 8; Gaps 5;
 QY 1 MDRSKENCISGPVKATAPVGGPKRVLVLTQOFPQNPPLPNSGQAQRVLCPSNSQSQRVPLQ 60
 Db 1 MDRCKENCYSRFVKSTVTF-GPKRVLVLTQOFPQNPPLPNSGQAQRVLCPSN-SQRVPPQ 58
 QY 61 AOKLVSSHPVQKQKQLOQATSVHPVSRPLNNTOKSKQPLPSAPENNPEELASKQKN 120
 Db 59 AOKPVAGQKPV----LKQLPAASGPRPASR-LSNPQKSEQPPQPAASGNSEKEQTSIQKT 113
 QY 121 EESKQRQWALEDFEIGRPLGKGFNGVYLAREKQSKFIALKLVFKQALEKAGVEHQLRR 180
 Db 114 EDSKQRQWLTDFDGRPLGKGFNGVYLAREKQSKFIALKLVFKVQLEKAGVEHQLRR 173
 QY 181 EVEIQSHLRHPNLRILGYFHDATRVYLILEVAPLGTVYRELOKLSKPFDEQRTATYITEL 240
 Db 174 EVEIQSHLRHPNLRILGYFHDATRVYLILEVAPLGTVYRELOKLSKPFDEQRTATYITEL 233
 QY 241 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPEM 300
 Db 234 ANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTTLCGLDYLPPEM 293
 QY 301 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYSKRISRVETFPDFVTEGARDLI 360
 Db 294 IEGRMHDEKVDLWSLGVLCYFELVGGKPPPEANTYQETYSKRISRVETFPDFVTEGARDLI 353
 QY 361 SRLLKHNPSQRMPLREVLHPWITANSSKPSNCKESASKOS 403
 Db 354 SRLLKHNPSQRMPLREVLHPWITANSSKPSNCKESASKOS 397
 RESULT 3
 ID Q8C3H8 PRELIMINARY; PRT; 386 AA.
 AC Q8C3H8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 DE library, clone:D830019B15 product:serine/threonine kinase 6, full
 DE insert sequence.
 GN Name=Stk6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carrincci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).


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RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsui S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima J., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numasaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitho H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tomaru A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK085861; BAC39557.1; -.
DR HSSP; Q14965; 10L6.
DR MGSD; G18945; 10L6.
DR HSP; G189478; Stk6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 43968 MW; 31970E9CDE31C6A7 CRC64;

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Query Match 78.7%; Score 1661.5; DB 2; Length 386;
Best Local Similarity 84.2%; Pred. No. 6.2e-98;
Matches 330; Conservative 16; Mismatches 37; Indels 9; Gaps 5;

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Db 112 EDTKRWMTLEDPDIGRPLGKGFNGVYLARERQSKFILALKVLFKTLQLEKANVEHQLRR 171
Qy 181 EYEIOHLRHPNLRILGYFHDATRVYLILEVAPLGTVVYRELQKLSKDFEQRTATYITEL 240
Db 172 EYEIOHLRHPNLRILGYFHDATRVYLILEVAPLGTVVYRELQKLSKDFEQRTATYITEL 231
Qy 241 ANALSYCHSKRVIHRDIPENLLGSGAGELKIADFGWSVHAPSSRRRTTLGGTLDYLPPEM 300
Db 232 ANALSYCHSKRVIHRDIPENLLGSGAGELKIADFGWSVHAPSSRRRTTLGGTLDYLPPEM 291
Qy 301 IEGRMHDEKVDLWSLGVLCYEFVGLVCKPPPEANTYQETKYISRVETFFDFVTEGARDLI 360
Db 292 IEGRMHDEKVDLWSLGVLCYEFVGLVCKPPPEANTYQETKYISRVETFFDFVTEGARDLI 351
Qy 361 SRLKHNPQSOREPLREVLEHPWITANSSKPSN 392
Db 352 SRLKHNPQSOREPLREVLEHPWITANSSKPSN 383

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RESULT 4

STK6 MOUSE STANDARD; PRT; 395 AA.

ID STK6 MOUSE STANDARD; PRT; 395 AA.

AC P97477; O35624; Q91YU4;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Aurora-family kinase 1)

DE 1) (Aurora/TP1-related kinase 1) (Ipl1- and aurora-related kinase 1)

DE (Aurora-A) (Serine/threonine kinase Aylk1).

GN Name=Stk6; Synonyms=Arkl, Aylk1, Iaki;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=BALB/C; TISSUE=Testis;

RX MEDLINE=97392693; PubMed=9245792; DOI=10.1083/jcb.138.3.643;

RA Gopalan G., Chan C.S.M., Donovan P.J.;

RT "A novel mammalian, mitotic spindle-associated kinase is related to yeast and fly chromosome segregation regulators.";

RL J. Cell Biol. 138:643-656(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=97349097; PubMed=9205101; DOI=10.1038/sj.onc.1201144;

RA Yanai A., Arama E., Kilfin G., Morro B.;

RT "ayk1, a novel mammalian gene related to Drosophila aurora centrosome separation kinase, is specifically expressed during meiosis.";

RL Oncogene 14:2943-2950(1997).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=BALB/C;

RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;

RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,

RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;

RT "cDNA cloning, expression, subcellular localization, and chromosomal assignment of mammalian aurora homologues, aurora-related kinase (ARK) 1 and 2.";

RT 1 and 2.";

RL Biochem. Biophys. Res. Commun. 244:285-292(1998).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Hapkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.O., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,


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Db 1 MDRCKENCVRPVKTTVPF-GPKRVLTVEQIPSONLGSSASSGOAQRVLPSPN-SQRVPSQ 58
Qy 61 AQLVSHKPVQKQKQLOATSVPHVPSRPLNNTQKSKQPLSPAPENNPEELASKQKN 120
Db 59 AQLGAGQKPA----KQLPAAVPRVSR-LNNPQKNEQ--DAAGNDSEKEQASLQKT 111
Qy 121 EESKKGWALEDFEIGRPGLGKGFNGVYLAREKSKFIALKVLKPAOLEKAGVEHQLR 180
Db 112 EDTKKGWLTLEDFDIPGLGKGFNGVYLAREKSKFIALKVLKPAOLEKANVEHQLRR 171
Qy 181 EVEIQSHLRHPNLRILRYGYFHDATRVYLILEYAPLGVTVVRELOKSKFDEORTATYITEL 240
Db 172 EVEIQSHLRHPNLRILRYGYFHDATRVYLILEYAPLGVTVVRELOKSKFDEORTYITEL 231
Qy 241 ANALSYCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAPSRRRTTCGLDYLPPEM 300
Db 232 ANALSYCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAPSRRRTTCGLDYLPPEM 291
Qy 301 IEGRMHDEKVDLSGLVLCYEFVGVGPPPEANTYQETRYKHSRVEFTFPDFVTEGARDLI 360
Db 292 IEGRMHDEKVDLSGLVLCYEFVGVGPPPEANTYQETRYKHSRVEFTFPDFVTEGARDLI 351
Qy 361 SRLLENKPSORPMLREVLHPMTANSSK-PSNCONKESASKOS 403
Db 352 SRLLENKPSORPMLREVLHPMTANSSK-PSNCONKESASKOS 395

RESULT 7
ST6L XENLA
ID ST6L XENLA STANDARD; PRT; 408 AA.
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Eg2-like (EC 2.7.1.37) (p46Xlbg22).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellac R., Paris J., Couturier A., Philippe M.;
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC -|- PTM: Phosphorylated (By similarity).
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cell cycle; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 140 390 Protein kinase.
FT NP_BIND 146 154 ATP (By similarity).
FT BINDING 169 169 ATP (By similarity).
FT ACT_SITE 263 263 Proton acceptor (By similarity).
SQ SEQUENCE 408 AA; 46461 MW; 97F6A69C7357AE8 CRC64;

Query Match 62.6%; Score 1320.5; DB 1; Length 408;
Best Local Similarity 66.5%; Pred. No. 3.5e-76;
Matches 286; Conservative 47; Mismatches 74; Indels 13; Gaps 6;

Qy 1 MDRS-KENCISGPKVATAPV-GGPKRVLTVPQPCQNPPLFVNSGOAQRVLPSPNSQSRVP 58
Db 1 MERAVKENHKPSNVKVFHPWTEGPKRI PVSQPPSTQVRPPTVGVSAQRILGPSNVQVRVM 60
Qy 59 LQAK-LVSSHKPVQKQKQLOATSVPHVPSRPLN-NTQKSKQPLSPAPENNPEELAS 116
Db 61 MQAKPVLNSQKPT---AQGLLRPATHGHTSKPQGNENRNPQQTSHSTPNMEKKGST 117
Qy 117 KO-----KNEESKKGWALEDFEIGRPGLGKGFNGVYLAREKSKFIALKVLKPAOLE 170
Db 118 DQKTLAVPKKEGKKQWCLDFEIGRPGLGKGFNGVYLAREKSKFIALKVLKFSQLE 177
Qy 171 KAGVEHQLRRVEIQSHLRHPNLRILRYGYFHDATRVYLILEYAPLGVTVVRELOKSKFDE 230
Db 178 KAGVEHQLAREVEIQSHLRHPNLRILRYGYFHDASRVYLILDYAPGGELFRELQKTRFDD 237
Qy 231 QRTATYITILANALSYCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAPSRRRTTLC 290
Db 238 QRSALYIKQALAEALYCHSKVKVTHRDIKPENLLGSGAGELKIADFGWSVHAPSRRRTTLC 297
Qy 291 GTLDYLPPEMIEGRMHDEKVDLSGLVLCYEFVGVGPPPEANTYQETRYKHSRVEFTFPD 350
Db 298 GTLDYLPPEMIEGRMHDEKVDLSGLVLCYEFVGVGPPPETDTHQETRYKHSRVEFTFPD 357
Qy 351 FVTEGARDLISRLLENKPSORPMLREVLHPMTANSSKP 390
Db 358 YVSEAKDLVSLKLNPNHRLPLKGVLEHPMIVKNSQQP 397

RESULT 8
Q6DJKO PRELIMINARY; PRT; 408 AA.
ID Q6DJKO PRELIMINARY; PRT; 408 AA.
AC Q6DJKO;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE LOC398349 protein.
GN Name=LOC398349;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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QY 1 MDRS-KENCISGPKATAPV-GGPKRVLTQQPCCQNPPLPVNSGQQRVLCPNSNQRPV 58
Db 1 MEBAVKENHKPSNVKIFHPMTEGAKIPVNPQOSTQFRPGTAVSAQRILGPSNVQPVL 60
QY 59 LQAKK-LVSSHKKVQKQKQLQATSVHPVPSPPLNNTOKSKQPLPSAPENNPPEELASK 117
Db 61 AQAKPILSSQKP-----TTQIP---LRPATGQHSSXKPPQPNENRNPQQTSHS 107
QY 118 QKN-----EESKQGWALEDFEIGRPLGKGFNGVNLAREKQSKFILA 160
Db 108 TPNVKKGSTDOCKTSAPVKECKKKQWCLDFEIGRPLGKGFNGVNLAREKSKFILA 167
QY 161 LKVLFAQLEKAGVEHQLRREVEIQSHLRHNPILRLYGYPHDAITRVILLEYAPLGTVVR 220
Db 168 LKVLFSQLEKAGVEHQLRREVEIQSHLRHNPILRLYGYPHDAITRVILLEYAPLGTVVR 227
QY 221 ELQKLSKDFEORTATYITELANALSCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVH 280
Db 228 ELQKCTFDDQDSAMYIKQAEALLYCHSKKVTHRDIKPENLLGSGAGELKIADFGWSVH 287
QY 281 APSRRTTLCGTLDPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYR 340
Db 288 APSRRTTLCGTLDPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYR 347
QY 341 ISRVETFPDFVTEGARDLISRLKKNPSPQRMPLREVLEHPMTTANS 387
Db 348 ISKVEFYQPPVSEARLDVSKLLKNPNHRLPLKGVLEHPWIKN 394

RESULT 10
Q6DBZ4
ID Q6DBZ4 PRELIMINARY; PRT; 405 AA.
AC Q6DBZ4;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DE Zgc:100912 protein.
GN Name=zgc:100912;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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CC -L- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC078304; AAH78304.1; -.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 405 AA; 45447 MW; B04793FC827BD489 CRC64;

Query Match 57.1%; Score 1204.5; DB 2; Length 405;
Best Local Similarity 60.7%; Pred. No. 8.6e-69;
Matches 242; Conservative 45; Mismatches 85; Indels 27; Gaps 6;

QY 4 SKENCISGPKATAPVGGPKRVLTQ--QFPCCNPPLPVNSGQAQ-----RVLCP 51
Db 10 SRDLKIHRENEKVSAAQPKRPVPTQSVQKPSNPHTRVLGAAGQPGQRPVGVKTS 69
QY 52 NSSQRPVLAQKLVSSHKKVQKQKQLQATSVHPVPSPPLNNT-QSKQPLPSAPEN 110
Db 70 QNTR-PEQ-----HKPAHKKPQ-----KPLSAETNKTAEPSKQDKPHQTP 115
QY 111 EEELASKQKNEKSKROWALEDFEIGRPLGKGFNGVNLAREKQSKFILA LKVLFA 170
Db 116 TSTSTNTSSGSSKSKKAWLENDFIGRALGKGFSGVYLAREQTFILALVKLFK 175
QY 171 KAGVEHQLRREVEIQSHLRHNPILRLYGYPHDAITRVILLEYAPLGTVVRLE 230
Db 176 KAGVEHQLRREVEIQSHLRHNPILRLYGYPHDAITRVILLEYAPLGTVVRLE 235
QY 231 QRTATYITELANALSCHSKRVTHRDIKPENLLGSGAGELKIADFGWSVHAP 290
Db 236 QRSATYIMELADALRYCHSKAVTHRDIKPENLLGSGAGELKIADFGWSVH 295
QY 291 GTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYRISRV 350
Db 296 GTLDYLPPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYRISRV 355
QY 351 FVTEGARDLISRLKKNPSPQRMPLREVLEHPMTTANSK 389
Db 356 HVSNGSRDLINRLKKNPMPHRLPIQGVMEHPWVVENSTK 394

RESULT 11
Q9DF70
ID Q9DF70 PRELIMINARY; PRT; 361 AA.
AC Q9DF70;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Protein kinase AIRK2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453769; PubMed=10996078; DOI=10.1016/S0960-9822(00)00673-4;
RA Adams R.R., Wheatley S.F., Gouldsworthy A.M., Kandels-Lewis S.E.,
RA Carmona M., Smythe C., Gerloff D.L., Barnshaw W.C.;
RT "INCENP binds the Aurora-related kinase AIRK2 and is required to

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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 361 AA; 41777 MW; 1FB77EF41ED07E8 CRC64;

Query Match      50.6%; Score 1067.5; DB 2; Length 361;
Best Local Similarity 55.6%; Pred. No. 4e-60;
Matches 212; Conservative 61; Mismatches 63; Indels 45; Gaps 8;

QY 35 NPLPVNSGQAVRLCPNS--SSQVPLQAKLVSSH-KPVQKQKQLQ-----ATS 83
DB 8 NP-----SSYTSKFTTSSATAQRV-LRKEPVVSTFTTSDNLLAQRTQLSRITPSASS 62
QY 84 VPHPVVS---RPLNNTQKSKQLPSAPENNPBEELASKQNEESKKQWALEDFEIGRPL 139
DB 63 VPGRAVAVSTEMPSONTALAEMP-----KRKFTIDDFDIGRPL 99
QY 140 GKGKFGNVYLAREKQSKFTIALKVLFPKAQLEKAGVEHQLRREVEIQSHLRHPNILRYGY 199
DB 100 GKGKFGNVYLAREKQSKFTIALKVLFPKSQLEKGEVHQLRREVEIQSHLRHPNILRYMY 159
QY 200 FHDATRVYLILEVAPLGTVYRELQKLSKPFDEORTATYITELANALSYCHSKRVIHRIK 259
DB 160 FHDRKRIYLMLEFAPRGELYKELQKHGRFDEQRSATFMEELADALHYCHERKVIHRDIK 219
QY 260 ENLLGSAGELKIADFGWSVHAPSSRRRTTCGLDYLPPMEIEGRMHDEKVDLWSLGVLC 319
DB 220 ENLLMGYKGLKIADFGWSVHAPSLRRRTTCGLDYLPPMEIEGKTHDEKVDLWCAGVLC 279
QY 320 YEFVLGKPPPEANTYQETKYRSRVETFPDFVTEGARDLISRLKXNPSQRPMLREVLE 379
DB 280 YEFVLGMPFPDPSHTEHRRIVNVLDKFPPLSDGSKDLISKLLRYHPQRLPLKGVME 339
QY 380 HPWITANSK--PSNCKNES 398
DB 340 HPWVKANSRRVLPVYVQSTQS 360

RESULT 15
Q6DE08 PRELIMINARY; PRT; 361 AA.
AC Q6DE08;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC398457 protein.
GN Name=LOC398457;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/advy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC077339; AAH77339.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 361 AA; 41735 MW; 384803072040015B CRC64;
```

Query Match 50.6%; Score 1067.5; DB 2; Length 361;
Best Local Similarity 55.6%; Pred. No. 4e-60;
Matches 212; Conservative 61; Mismatches 63; Indels 45; Gaps 8;

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QY 35 NPLPVNSGQAVRLCPNS--SSQVPLQAKLVSSH-KPVQKQKQLQ-----ATS 83
DB 8 NP-----SSYTSKFTTSSATAQRV-LRKEPVVSTFTTSDNLLAQRTQLSRITPSASS 62
QY 84 VPHPVVS---RPLNNTQKSKQLPSAPENNPBEELASKQNEESKKQWALEDFEIGRPL 139
DB 63 VPGRAVAVSTEMPSONTALAEMP-----KRKFTIDDFDIGRPL 99
QY 140 GKGKFGNVYLAREKQSKFTIALKVLFPKAQLEKAGVEHQLRREVEIQSHLRHPNILRYGY 199
DB 100 GKGKFGNVYLAREKQSKFTIALKVLFPKSQLEKGEVHQLRREVEIQSHLRHPNILRYMY 159
QY 200 FHDATRVYLILEVAPLGTVYRELQKLSKPFDEORTATYITELANALSYCHSKRVIHRIK 259
DB 160 FHDRKRIYLMLEFAPRGELYKELQKHGRFDEQRSATFMEELADALHYCHERKVIHRDIK 219
QY 260 ENLLGSAGELKIADFGWSVHAPSSRRRTTCGLDYLPPMEIEGRMHDEKVDLWSLGVLC 319
DB 220 ENLLMGYKGLKIADFGWSVHAPSLRRRTTCGLDYLPPMEIEGKTHDEKVDLWCAGVLC 279
QY 320 YEFVLGKPPPEANTYQETKYRSRVETFPDFVTEGARDLISRLKXNPSQRPMLREVLE 379
DB 280 YEFVLGMPFPDPSHTEHRRIVNVLDKFPPLSDGSKDLISKLLRYHPQRLPLKGVME 339
QY 380 HPWITANSK--PSNCKNES 398
DB 340 HPWVKANSRRVLPVYVQSTQS 360
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RESULT 16

072YT9 PRELIMINARY; PRT; 371 AA.
 AC Q7ZYT9
 DT 01-JUN-2003 (TEMBLrel. 24, Created)
 DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE LOC398457 protein (Fragment).
 GN Name=LOC398457;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Udín T.B., Tohiyuki S., Carninci P., Abrahams R.D.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC041288; AAH41288.1; --
 DR HSSP; O14965; 10L6.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR007119; Prot kinase.
 DR InterPro; IPR002290; Ser/Thr kinase.
 DR InterPro; IPR008271; Ser/Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; I.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc_1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 371 AA; 42716 MW; 19F0C009D0838CFC CRC64;

Query Match

50.6%; Score 1067.5; DB 2; Length 371;

Best Local Similarity 55.6%; Pred. No. 4.1e-60;
 Matches 212; Conservative 61; Mismatches 63; Indels 45; Gaps 8;
 QY 35 NPLPVNSGQARVLCPSN--SSQVPLQAKGVSSH-KPVQNKQKQLQ-----ATS 83
 DB 18 NP---SSYTSKFTTSSATAAQRV-LRKEPVYSTFTTSDNLLAQRTLSRTPSSASS 72
 QY 84 VHPVPS-----RPLNNTQSKQPLSPAPENNPEELASKQKQVESKQKQWALEDFEIGRPL 139
 DB 73 VPGRVAVSTEMPSONTALAEMP-----RRKFTIDDFDIGRPL 109
 QY 140 GKKGFGNVYLAREKQSKFIALKVLKFAQLKAGVEHQLRREVEIOSHLRHPNLRVLYGY 199
 DB 110 GKKGFGNVYLAREKQSKFIALKVLKFAQLKAGVEHQLRREVEIOSHLRHPNLRVLYGY 169
 QY 200 FHDATRVYLILEYAPLGTGVYVRELQKLSKFDQRTATYITELANALSYCHSKRVVHRDIKP 259
 DB 170 FHDKRKIYLMLEFAPRGELYKELQKHGRFDEQSRATFMEELADALHYCHERKVIHRDIKP 229
 QY 260 ENLLISAGELKIADFGWSVHAPSSRRRTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLC 319
 DB 230 ENLLMGYKGLKIADFGWSVHAPSSRRRTLCGTLDYLPPEMIEGRMHDEKVDLWSLGVLC 289
 QY 320 YEFVLCKPPEANTYQETKYRISRVFTFPDPVTEGARDLISRLKHPNPSQRMPLREVLE 379
 DB 290 YEFVLCKPPEANTYQETKYRISRVFTFPDPVTEGARDLISRLKHPNPSQRMPLREVLE 349
 QY 380 HPWITANSSK--PSNCKNKS 398
 DB 350 HPWVKANSRRVLPVYVQSTQS 370
 RESULT 17
 AURB MOUSE STANDARD; PRT; 345 AA.
 ID AURB MOUSE STANDARD; PRT; 345 AA.
 AC 070126; Q61882;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora-related
 DE kinase 2) (Serine/threonine-protein kinase 5) (STK-1) (Aurora-B).
 GN Name=Aurkb; Synonyms=Ark2, Stk1, Stk12, Sck5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=96194801; PubMed=8647446; DOI=10.1016/0378-1119(95)00809-8;
 RA Niwa H., Abe K., Kunitada T., Yamamura K.;
 RT "Cell-cycle-dependent expression of the STK-1 gene encoding a novel
 RT murine putative protein kinase";
 RL Gene 169:197-201(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2";
 RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Udín T.B., Tohiyuki S., Carninci P., Abrahams R.D.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC041288; AAH41288.1; --
 DR HSSP; O14965; 10L6.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR007119; Prot kinase.
 DR InterPro; IPR002290; Ser/Thr kinase.
 DR InterPro; IPR008271; Ser/Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; I.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc_1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 1
 SQ SEQUENCE 371 AA; 42716 MW; 19F0C009D0838CFC CRC64;

RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalilus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";	Db	105	REIVALKILFKSQIEKEGVEHQRLREIEIOAHLKHPNIOQLNYFYDQQRVILEYAPR	164
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	Qy	216	GTVYRELQKLSKDFEORTATYITELANALYSCHSKSVIRHDIKPNELLIGSAGELKIADF	275
CC	-I- FUNCTION: May be directly involved in regulating the cleavage of polar spindle microtubules and is a key regulator for the onset of cytokinesis during mitosis (By similarity).	Db	165	GBLYELQKSRFTDEQRTATIMEELSDALTYCHKKVIRHDIKPNELLIGLOQELKIADF	224
CC	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	Qy	276	GWSVHAPSRRRTTLCGTLDYLPPEMTEGRMHDKVDLSGLVLCYEFVGLGKPPFEANTYQ	335
CC	-I- SUBCELLULAR LOCATION: Localized to the midzone of central spindle in late anaphase and concentrated into the midbody in telophase and cytokinesis. Colocalized with gamma tubulin in the mid-body (By similarity).	Db	225	GWSVHAPSURRTKMTCTDYLPPMEIEGRHNMVDLMCIQVLCYELMVGNPFPFSPSHS	284
CC	-I- TISSUE SPECIFICITY: Expressed in testis, intestine and spleen. All of them are tissues that contain a large number of proliferating cells. Expressed during S phase, in a cell-cycle-dependent fashion.	Qy	336	ETVYKISRISVETFPDFVTEGARDLSRLKHPNQSPQRLREVLHHPWITANSK	389
CC	-I- DEVELOPMENTAL STAGE: Strongly expressed in 8.5 and 12.5 dpc.	Db	285	ETVYRIVKVDLKPFPSSVPSGAQDLISKLLKNPQRLPLAEVAHPWVRANSRR	338
CC	-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora subfamily.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
DR	EMBL; D21099; BAA04658.1; --				
DR	EMBL; U69107; AAC12683.1; --				
DR	EMBL; BC003261; AA003261.1; --				
DR	HSSP; P31751; 1GZK.				
DR	MGI; MGI:107168; Aurkb.				
DR	InterPro; IPR011009; Kinase like.				
DR	InterPro; IPR000719; Prot_kinase.				
DR	InterPro; IPR008271; Ser_thr_pkin_AS.				
DR	Pfam; PF00069; Pkinase; 1.				
DR	ProDom; PD000001; Prot_kinase; 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
KW	ATP-binding; Cell cycle; Serine/threonine-protein kinase; Transferase.				
FT	DOMAIN 82 332				
FT	BP BIND 88 96				
FT	BP BIND 111 111				
FT	ACT_SITE 205 205				
FT	CONFLICT 44 44				
SQ	SEQUENCE 345 AA; 39324 MW; C1D1DB8BDEA00A0 CRC64;				
	Query Match 50.3%; Score 1061; DB 1; Length 345;				
	Best Local Similarity 59.0%; Pred. No. 9.7e-60;				
	Matches 209; Conservative 48; Mismatches 73; Indels 24; Gaps 4;				
Qy	36 PLPVNSGQQRVLCPNSSQRVPLQAKLVSSHKPVQNKQKQLQATSVHPVPSPLNNT	95			
Db	9 PWPYGSKTSQSGI--NTLSQRV-----LRKEPATTSALVNR--SNS	47			
Qy	96 QKSKQPLSPAPENNPEELASQKNEESKROWALEDEIRIGPLGKFGNVLAREKOS	155			
Db	48 QSTAPGQKLAENKSGSTGQ---GQNKQPTIDNFEIRGLPGKFGNVLAREKKS	104			
Qy	156 KFTLALKVLFKAQLEKAGVEHQRLREVEIQSHLRHPNIIRLLYGYFHDATRVVILEYAPL	215			

RESULT 18

AURB HUMAN

ID AURB HUMAN STANDARD; PRT; 344 AA.

AC Q96GD4; O14630; O60446; O95083; Q96DV5; Q9UQ46;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-

DE like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase

DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).

GN Name-AURKB; Synonyms-AIK2, AIM1, ARK2, STK12;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;

RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,

RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;

RT "cDNA cloning, expression, subcellular localization, and chromosomal

RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)

RT 1 and 2.";

RL Biochem. Biophys. Res. Commun. 244:285-292(1998).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99025855; PubMed=9809983;

RA Tatsuoka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,

RA Terada Y.;

RT "Multinuclearity and increased ploidy caused by overexpression of the

RT aurora- and Ipl1-like midbody-associated protein mitotic kinase in

RT human cancer cells.";

RL Cancer Res. 58:4811-4816(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver, and Spleen;

RX MEDLINE=99077743; PubMed=9858806;

RA Kimura M., Matsuda Y., Yoshioka T., Sumi N., Okano Y.;

RT "Identification and characterization of STK12/Aik2: a human gene

RT related to aurora of Drosophila and yeast IPL1.";

RL Cytogenet. Cell Genet. 82:147-152(1998).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=21364697; PubMed=11471245;

RA Prigent C., Gill R., Tower M., Sanseau P.;

RT "In silico cloning of a new protein kinase, Aik2, related to

RT Drosophila aurora using the new tool: EST Blast.";

RL In Silico Biol. 1:123-128(1999).

RN [5]

RP SEQUENCE FROM N.A.

RA Zhang Q., Yu L., Bi A.;

RT "Cloning of a novel human gene homologous to mouse STK-1.";

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung, Lymph, and Muscle;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klaesner R.D., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toohily S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [7]

RN REVIEW.

RP MEDLINE=21306577; PubMed=11413462; DOI=10.1038/35048096;

RX Nigg E.A.;

RT "Mitotic kinases as regulators of cell division and its checkpoints."; Nat. Rev. Mol. Cell Biol. 2:21-32(2001).

RL FUNCTION: May be directly involved in regulating the cleavage of polar spindle microtubules and is a key regulator for the onset of cytokinesis during mitosis.

CC -!

CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -! SUBCELLULAR LOCATION: Localized to the midzone of central spindle in late anaphase and concentrated into the midbody in telophase and cytokinesis. Colocalized with gamma tubulin in the mid-body.

CC -! TISSUE SPECIFICITY: High level expression seen in the thymus. It is also expressed in the spleen, lung, testis, colon, placenta and fetal liver. Expressed during S and G2/M phase and expression is up-regulated in cancer cells during M phase.

CC -! DISEASE: Disruptive regulation of expression is a possible mechanism of the perturbation of chromosomal integrity in cancer cells through its dominant-negative effect on cytokinesis.

CC -! SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora subfamily.

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CC -----

CC EMBL; AF008552; AAC12709.1; -

CC EMBL; AB011450; BAA32136.1; -

CC EMBL; AB011446; BAA82709.1; -

CC EMBL; AF004022; AAB65786.1; -

CC EMBL; AF015254; AAC98891.1; -

CC EMBL; BC000442; AAH00442.2; ALT_INIT.

CC EMBL; BC009751; AAH09751.1; -

CC EMBL; BC013300; AAH13300.2; ALT_INIT.

CC HSSP; P31751; IGZK.

CC Genew; HGNC:11390; AURKB.

CC H-InVDB; HIX0019005; -

CC MIM; 604970; -

CC InterPro; IPR011009; Kinase like.

CC InterPro; IPR000719; Prot kinase.

CC InterPro; IPR002230; Ser_Thr_kinase.

CC InterPro; IPR008271; Ser_Thr_kin_AS.

CC Pfam; PF00069; Pkinase; 1.

CC ProDom; PD000001; Prot kinase; 1.

CC SMART; SM00220; S_TKc; 1.

CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Cell cycle; Serine/threonine-protein kinase; Transferase.

FT DOMAIN 77 327 Protein kinase.

FT NP BIND 83 91 ATP (By similarity).

FT BINDING 106 106 ATP (By similarity).

FT ACT SITE 200 200 Proton acceptor (By similarity).

FT CONFLICT 14 15 RQ -> DK (in Ref. 5).

FT CONFLICT 70 70 R -> MR (in Ref. 6; AAH13300).

FT CONFLICT 161 161 E -> M (in Ref. 4 and 5).

FT CONFLICT 167 169 QKS -> HKT (in Ref. 4).

FT CONFLICT 179 179 T -> TVRR (in Ref. 4).

FT CONFLICT 180 180 I -> VRAY (in Ref. 5).

FT CONFLICT 226 226 P -> T (in Ref. 3).

FT CONFLICT 249 250 MH -> ID (in Ref. 3).

FT CONFLICT 271 271 Missing (in Ref. 3).

FT CONFLICT 298 298 T -> M (in Ref. 6; AAH09751/AAH13300).

SQ SEQUENCE 344 AA; 39280 MW; 8325E3EF5A1FB170 CRC64;

Query Match 50.1%; Score 1057.5; DB 1; Length 344;

Best Local Similarity 63.2%; Pred. No. 1.6e-59;

Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSRLNNTQSKQPL-PSA-----PENNPEELASKOKNEESKK-----ROWA 129

DB 22 STLQPVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMENSGTDPDLTRHFT 73

QY 130 LDFEIGRPLGKGNVYLAREKSKFILAUKVLPAQLEKAGVHQLRREVEIOSHLR 189

DB 74 IDDFEIGRPLGKGNVYLAREKSKSHFVALVKLFKSIQIEKGEVHQLRREIEIOAHLH 133

QY 190 HNNILRLCYGFHDATRVYLLEVPGLTVYVRELOKLSKFEDEORTATVITELANALSYCHS 249

DB 134 HNNILRLYNYFYDRRIYLLIYAPRGELYKELQSKCTFDEORTATIMBELADALMYCHG 193

QY 250 KVIHRIKPNELLGSGAGELKIAFGWSVHAPSSRRRTTCGLTDLVLPPEMIEGRMHDEK 309

DB 194 KVIHRIKPNELLGSGAGELKIAFGWSVHAPSSRRRTTCGLTDLVLPPEMIEGRMHNEK 253

QY 310 VDLWSLGVLCYFLVCKGPPFEANTYKRSRVEFTTDFPDFTVGARDLISLLKHNPSS 369

DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVKVDLPKPPASVPTGAQDLISKLRHNPSS 313

QY 370 QRPMLREVLEHVPWITANSKK---PSNCON 395

DB 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 19

Q8C6C1 PRELIMINARY; PRT; 345 AA.

AC Q8C6C1

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410042H09 product:serine/threonine kinase 5, full insert sequence.

DE sequence.

GN Name=Aurkb;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

"Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Iehii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toyota T., Yamamura T., Yamanaka I., Yasunishi A.,
 RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK075951; BAC36078.1; -;
 DR HSSP; O14965; 1OL6
 DR MGD; MGI:107168; Aurkb.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPRO11009; Kinase like.
 DR InterPro; IPRO20252; N6_Mtase.
 DR InterPro; IPRO00719; Prot_kinase.
 DR InterPro; IPRO02290; Ser_thr_pkinase.
 DR InterPro; IPRO08271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC_1
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 345 AA; 33384 MW; D204D891CF00A4 CRC64;

Matches 209; Conservative 47; Mismatches 74; Indels 24; Gaps 4;
 QY 36 PLPVNSGOAQRVLCPSNSQSRVPLQAKLVSSHKPVQKOKLOQATSVHPVPSRPLNNT 95
 Db 9 PWPYGSKTSQSL--NTLSQRV-----LRKEPATTSALVNR--FNS 47
 QY 96 QKSQOPLSPAPENPEELASOKNEESKKRQWALDEFEIGRPLGKGGNVLAREKOS 155
 Db 48 QSTAAPGQKLAENKSGGSTAQ---GSKNQKFTIDNFEIGRPLGKGGNVLAREKKS 104
 QY 156 KFILALKVLFKAQLEKAGVEHQIRREVEIQSHLRHPNLRILYGYFHDAFVVLILEYAPL 215
 Db 105 RFIVALKILFKSQIEKGEVHQIRREIEIQAHKHPNLRILYGYFHDAFVVLILEYAPR 164
 QY 216 GTVYRELQKLSKFDQRTATYITELANALSYCHSKRVIRHDIKPNLLIGSAGELKIADP 275
 Db 165 GELYELQKSRFDQRTATIMEELSDALTYCHKKKVIHRDIKPNLLIGLOGLKIADP 224
 QY 276 GWSVHAPSRRRTTLCTGLDYLPPMIEGRMHDKVDLSGLVLCYEFVLGKPPFEANTYQ 335
 Db 225 GWSVHAPSLRRKTMCGTLDYLPPMIEGRMHENVDLWLCIGVLCYELMVGNDPFPSPSHS 284
 QY 336 EYKISRISVEFTFPFVTEGARDLISRLKHPNSQRPMLREVLHPWITANSK 389
 Db 285 EYRRIRVVDLKFPPSPVPSGAQDLISKLKHNPQRLPLAEVAHPWVRANSRR 338
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 ID_AURB_RAT STANDARD; PRT; 343 AA.
 AC O55099;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
 DE like midbody-associated protein 1) (AIM-1) (Aurora-B).
 GN Name=Aurkb; Synonyms=Aim1, Stk12;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=98119810; PubMed=9450992; DOI=10.1093/emboj/17.3.667;
 RA Terada Y., Tatsuoka M., Suzuki F., Yasuda Y., Fujita S., Otsu M.;
 RT "AIM-1: a mammalian midbody-associated protein required for
 RT cytokinesis.";
 RL EMBO J. 17:667-676(1998).
 CC -1- FUNCTION: May be directly involved in regulating the cleavage of
 CC polar spindle microtubules and is a key regulator for the onset of
 CC cytokinesis during mitosis (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
 CC in late anaphase and concentrated into the midbody in telophase
 CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
 CC (By similarity).
 CC -1- TISSUE SPECIFICITY: High level expression seen in the testis. It
 CC is also expressed in the spleen, lung and heart. Expressed in the
 CC G2/M phase of the cell cycle.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
 CC subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D89731; BAA23794.1; -;
 DR HSSP; P31751; 1GZK.

Query Match 50.1%; Score 1057; DB 2; Length 345;
 Best Local Similarity 59.0%; PBL; No. 1.8e-59;

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DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S TKC; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 344 AA; 39441 MW; 4DD7158CF2F5D047 CRC64;

Query Match 49.5%; Score 1045; DB 2; Length 344;
Best Local Similarity 56.9%; Pred. No. 1e-58;
Matches 209; Conservative 44; Mismatches 68; Indels 46; Gaps 5

Qy 32 PCQNPLPVNSGQQRVLCPNSSQRVPLQAKLVSSHKPVQNKQKQLQATSVPHPVSRP 91
Db | ||| |||| : : : || : : : || : : : || : : : ||
Qy 19 PGLNTLP-----QRVL-----RKPEVTPSALV-----LMSRSNAQPTAAP 53
Db | ||| |||| : : : || : : : || : : : || : : : ||
Qy 92 LNNQTSKQKPLPAPENNPPEELASKQKNESKKRWALEDFEIGRPLGKGKFGNVYLAR 151
Db || : : : || : : : || : : : || : : : || : : : || : : : ||
Qy 54 GQKVENSSTGNIP-----KRSFTIDDFEIGRPLGKGKFGNVYLAR 95
Db || : : : || : : : || : : : || : : : || : : : || : : : ||
Qy 152 EKOSKFTLALKLVFKAOLEKAGVEHQRLRREVEIQSHLRHPNILRLYGYFHDATRVYLLE 211
Db || : || : || : || : || : || : || : || : || : || : || : ||
Qy 96 EKSKHFIVALKLVFKSQIEKEGVEHQRLRRIEIQAHLOHPNILRLYNYFYDRRIYIJLLE 155
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 212 YAPLGTVYRELQKLSPDEQRTATYITELANALSYCHSKRVIHRIKIPENLLLSAGELK 271
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 156 YAPRGELYKELQSRTPDEQRTATIMEELADALTYCHAKKVIHRIKIPENLLLGRLGELK 215
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 272 IADFGSVHAPSRRRTILCTGLDYLPEMTEGRMHDEKVDLWSLGVLCYEFELGKPPPEA 331
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 216 IADFGSVHAPSRLRRKTMCGTLDYLPPEMTEGRTHNEKVDLWCTGVLCYELLGNPPFES 275
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Qy 332 NTYQETVKRISRYVEFTPDFVTEGARDLISRLKHNPQSQRPMLEVLHPMTANSSK-- 389
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 276 ASHWETVRRIVKVDLKEPPSPVPGAQFIYKLLKHNFSERLPLAQVSAHPWVRTHSRVL 335
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 390 -PSNCQN 395
Db || : || : || : || : || : || : || : || : || : || : ||
Qy 336 PPSAPQS 342

Search completed: June 20, 2005, 20:12:24
Job time : 141.649 secs

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Job time : 141.649 secs

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Q7YRC6
ID Q7YRC6 PRELIMINARY; PRT; 344 AA.
AC Q7YRC6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Serine/threonine kinase 12.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Li W., Yu L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR HMBL; AY336975; AAQ16151.1; -.
DR HSSP; O14965; 1OL6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR02052; N6_Mtase.
DR InterPro; IPR000719; Prot_kinase.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:59:50 ; Search time 37.7617 Seconds
(without alignments)
680.035 Million cell updates/sec

Title: US-10-734-126-3
Perfect score: 1809
Sequence: 1 MAQKENSYPWYGRQTAPSG.....PWYRNSRRVLPSPALQSV 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%
Maximum Match 100%
Listing first 65000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	344	2	US-08-755-728-3
2	1809	100.0	344	2	US-08-974-655-3
3	1809	100.0	344	3	US-09-283-011-3
4	1809	100.0	344	4	US-09-012-135A-3
5	1809	100.0	363	4	US-09-949-016-9826
6	1797.5	99.4	347	2	US-09-016-000-1
7	1520.5	84.1	343	4	US-09-485-534-4
8	1057.5	58.5	403	2	US-08-755-728-4
9	1057.5	58.5	403	2	US-08-974-655-4
10	1057.5	58.5	403	3	US-09-283-011-4
11	1057.5	58.5	403	4	US-09-012-135A-4
12	1057.5	58.5	488	4	US-09-949-016-10461
13	1057.5	58.5	488	4	US-09-949-016-10462

ALIGNMENTS

RESULT 1
US-08-755-728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, Gregory
; APPLICANT: MOSEIE, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-755-728-3

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Best Local Similarity 100.0%; Pred. No. 4.1e-176;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	SSGTPDILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVEH	120
Db	61	SSGTPDILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVEH	120
Qy	121	QLRRREIQAHLHPNLRNYFYDPRRRYLLILEVAPRGELKELQKCTFDEQRTATI	180
Db	121	QLRRREIQAHLHPNLRNYFYDPRRRYLLILEVAPRGELKELQKCTFDEQRTATI	180
Qy	181	MEELADALMYCHGKVKVHRDIPENLLGLKGELKIADFGWSVHAPSLRRTKCTGTLUDYL	240
Db	181	MEELADALMYCHGKVKVHRDIPENLLGLKGELKIADFGWSVHAPSLRRTKCTGTLUDYL	240
Qy	241	PPMIEGRMHNKVDLWCIGVLCYELLVGNPPPPESASHNETYRRIKVKDLKFPASVPTGA	300
Db	241	PPMIEGRMHNKVDLWCIGVLCYELLVGNPPPPESASHNETYRRIKVKDLKFPASVPTGA	300
Qy	301	QDLISKLLRHNPSERLPLAQVSAHPWYRNSRRVLPSPALQSV 344	
Db	301	QDLISKLLRHNPSERLPLAQVSAHPWYRNSRRVLPSPALQSV 344	

RESULT 2

US-08-974-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-974-655-3

Query Match 100.0%; Score 1809; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.1e-176;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTSPALVMSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTSPALVMSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPDLTRHFTIDDFEIGRPLGKFGNVYLAREKSHFIVALKVLPKSKQIEKEGVHEH 120
DB 61 SSGTDPDLTRHFTIDDFEIGRPLGKFGNVYLAREKSHFIVALKVLPKSKQIEKEGVHEH 120
QY 121 QLRREIEIQAHLPNIRLYNYFYDRRRYLYLILEYAPRGELYKELQKSTFDEQRTATI 180
DB 121 QLRREIEIQAHLPNIRLYNYFYDRRRYLYLILEYAPRGELYKELQKSTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKTADFQWSVHAPSLRRKKTTCGTLIDYL 240
DB 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKTADFQWSVHAPSLRRKKTTCGTLIDYL 240

QY 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
DB 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
RESULT 3
US-09-283-011-3
; Sequence 3, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-283-011-3

Query Match 100.0%; Score 1809; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.1e-176;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTSPALVMSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTSPALVMSRSNVQPTAAPGQKVMEN 60

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QY 121 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 180
DB 121 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKIADFGWSVHAPSRLRKTWCGLDYL 240
DB 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKIADFGWSVHAPSRLRKTWCGLDYL 240
QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
QY 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 4

US-09-012-135A-3
; Sequence 3, Application US/09012135A
; Patent No. 6716575
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6716575ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-012-135A-3

Query Match 100.0%; Score 1809; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.1e-176;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
DB 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
QY 121 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 180
DB 121 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKIADFGWSVHAPSRLRKTWCGLDYL 240
DB 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGBELKIADFGWSVHAPSRLRKTWCGLDYL 240
QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
QY 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 5

US-09-949-016-9826
; Sequence 9826, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9826
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9826

Query Match 100.0%; Score 1809; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 4.4e-176;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKVMEN 60
DB 20 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKVMEN 79
QY 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
DB 80 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 139
QY 121 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 180
DB 140 QLRREIEIOAHLHPNLRILYNYFYDRRIYLLILEYAPRGELYKELQKSCCTFDEQRTATI 199

QY 181 MEELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 240
DB 200 MEELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 259
QY 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVPTCA 300
DB 260 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVPTCA 319
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
DB 320 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 363

RESULT 6
US-09-016-000-1
; Sequence 1, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Gugler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,000
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HMCINOT01
; CLONE: 2940

US-09-016-000-1
Query Match 99.4%; Score 1797.5; DB 2; Length 347;
Best Local Similarity 99.1%; Pred. No. 6.2e-175;
Matches 344; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 MAQKENSYPWPGYGRQTAPSGLSTLPQVLRKEPVTSPALVMSRNSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPGYGRQTAPSGLSTLPQVLRKEPVTSPALVMSRNSNVQPTAAPGQKVMEN 60

QY 61 SSGTPOILTRHFTIIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSQIEKGVGH 120
DB 61 SSGTPOILTRHFTIIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSQIEKGVGH 120
QY 121 QURREIEIQAHLLHNPILRLYNYFYDRRIYILILEYAPRGELYKELQKCTFDEQRTAT- 179
DB 121 QURREIEIQAHLLHNPILRLYNYFYDRRIYILILEYAPRGELYKELQKCTFDEQRTATV 180
QY 180 --IMEELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 237
DB 181 RAIMBELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 240
QY 238 DYLPPMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVP 297
DB 241 DYLPPMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVP 300
QY 298 TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
DB 301 TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 347

RESULT 7
US-09-485-534-4
; Sequence 4, Application US/09485534
; Patent No. 6759212
; GENERAL INFORMATION:
; APPLICANT: TATSUKA, MASAAKI
; APPLICANT: TERADA, YASUHIKO
; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS
; FILE REFERENCE: 050499/0102
; CURRENT APPLICATION NUMBER: US/09/485,534
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/JF98/03641
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 235371/1997
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-485-534-4

Query Match 84.1%; Score 1520.5; DB 4; Length 343;
Best Local Similarity 84.5%; Pred. No. 1.1e-146;
Matches 290; Conservative 20; Mismatches 30; Indels 3; Gaps 1;
QY 1 MAQKENSYPWPGYGRQTAPSGLSTLPQVLRKEPVTSPALVMSRNSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPGYGRQTAPSGLSTLPQVLRKEPVTSPALVMSRNSNVQPTAAPGQKVMEN 60
QY 61 SSGTPOILTRHFTIIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSQIEK 117
DB 61 KGATALQGSQSRQPTTIDNFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSQIEK 120
QY 118 VEHQLRREIEIQAHLLHNPILRLYNYFYDRRIYILILEYAPRGELYKELQKCTFDEQRT 177
DB 121 VEHQLRREIEIQAHLLHNPILRLYNYFYDRRIYILILEYAPRGELYKELQKCTFDEQRT 180
QY 178 ATIMEELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 237
DB 181 ATIMEELADALMYCHGKVIHREDIKPENLLGLKGLKADFGWSVHAPSLRRKTCMTGTL 240
QY 238 DYLPPMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVP 297
DB 241 DYLPPMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKVDLKFPASVP 300
QY 298 TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPAL 340
DB 301 LGAKDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPAL 343

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RESULT 8
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-4

Query Match 58.5%; Score 1057.5; DB 2; Length 403;
Best Local Similarity 63.2%; Pred. No. 2.5e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQVRVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
DB 82 TSVPHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQKNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFQGVNVLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFQGVNVLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
QY 134 HNNILLYNYFYDRRIYILLEYAPRGELYKELQKSCFDEQRTAIMBELADALMYCHG 193
DB 190 HNNILLYGYFHDATRYVILEYAPRTGYVYRELOKLSKFDEQRTATYITELANALSYCHS 249

QY 194 KKVIRHDIKPNLLGLKELKIADFGWSVHAPSLRRTKTCGTLDTLPPMIEGRMHNEK 253
DB 250 KKVIRHDIKPNLLGLKELKIADFGWSVHAPSLRRTKTCGTLDTLDTLPPMIEGRMHNEK 309

QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKEPPASVPTGAQDLISLKLHNPS 313
DB 310 VDLWSGLVLCYELFVGVKPPPEANTYQETKYRISRVFTPPDFVTEGARDLISLKLHNPS 369

QY 314 ERLPLAQVSAHPWVRANSRRVLPPPSALQS 342
DB 370 QRPMLREVLEHPWITANSK---PSNCQN 395

RESULT 9
US-08-974-655-4
; Sequence 4, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-974-655-4

Query Match 58.5%; Score 1057.5; DB 2; Length 403;
Best Local Similarity 63.2%; Pred. No. 2.5e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQVRVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
DB 82 TSVPHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQKNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFQGVNVLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFQGVNVLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
QY 134 HNNILLYNYFYDRRIYILLEYAPRGELYKELQKSCFDEQRTAIMBELADALMYCHG 193
DB 190 HNNILLYGYFHDATRYVILEYAPRTGYVYRELOKLSKFDEQRTATYITELANALSYCHS 249

QY 194 KKVIRHDIKPNLLGLKELKIADFGWSVHAPSLRRTKTCGTLDTLPPMIEGRMHNEK 253
DB 250 KKVIRHDIKPNLLGLKELKIADFGWSVHAPSLRRTKTCGTLDTLDTLPPMIEGRMHNEK 309
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Db 130 LEDFEIGRPLGKGFNGVYLAREKQSKFIALKVLFAKLEKAGVHQHQRREVEIQSHLR 189
Qy 134 HPNILRLNRYFYDRRIYLLILEVAPRGELYKELQKCTDEQRTATIMEELADALMYCHG 193
Db 190 HPNILRLYGFHDATRVYLILEVAPLGTVYRELOKLSKFDEQRTATITELANALSYCHS 249
Qy 194 KKVIHRIKPNENLLGLKGBELKIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMNEK 253
Db 250 KKVIHRIKPNENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMDEK 309
Qy 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSLGVLCYELFVGNKPPFEANTYQETKYRISRVFTFPDFVTEGARDLISRLLKHNS 369
Qy 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLEHPWITANSK---PNSCQN 395

RESULT 10

US-09-283-011-4
; Sequence 4, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-09-283-011-4
Query Match 58.5%; Score 1057.5; DB 3; Length 403;
Best Local Similarity 63.2%; Pred. No. 2.5e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
Qy 22 STLPRVLR-----KEPVTFSALVLSRSNVQPTAAPGOKVMENSSTGTPDILTRHFT 73
Db 82 TSVPHVPSPLNNTQSKQPL-PSA-----PENNPEELASKQKNEESKK-----ROWA 129
Qy 74 IDDFEIGRPLGKGFNGVYLAREKQSHFIVALKVLFKSOIEKEGVHQHQRREIEIOAHIL 133
Db 130 LEDFEIGRPLGKGFNGVYLAREKQSKFIALKVLFAKLEKAGVHQHQRREVEIQSHLR 189
Qy 134 HPNILRLNRYFYDRRIYLLILEVAPRGELYKELQKCTDEQRTATIMEELADALMYCHG 193
Db 190 HPNILRLYGFHDATRVYLILEVAPLGTVYRELOKLSKFDEQRTATITELANALSYCHS 249
Qy 194 KKVIHRIKPNENLLGLKGBELKIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMNEK 253
Db 250 KKVIHRIKPNENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMDEK 309
Qy 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSLGVLCYELFVGNKPPFEANTYQETKYRISRVFTFPDFVTEGARDLISRLLKHNS 369
Qy 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLEHPWITANSK---PNSCQN 395

RESULT 11

US-09-012-135A-4
; Sequence 4, Application US/09012135A
; Patent No. 6716575
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 6716575ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-012-135A-4

Query Match      58.5%; Score 1057.5; DB 4; Length 403;
Best Local Similarity 63.2%; Pred. No. 2.3e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY  22 STLPQVLR-----KEPVTSPALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
DB  82 TSPVHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 129

QY  74 IDDFEIGRPLGKGFQNVYLAREKKSHFIVALKVLFKSKQIEKEGVHQLRRRETEIOAHILH 133
DB  130 LEDFEIGRPLGKGFQNVYLAREKQSKFILALKVLFKAQLEKAGVHQLRRRETEIOASHLR 189

QY  134 HPNILRLYNYFYDRIIRYILLEYAPRGELYKELQKSCTFDEQRTATIMBELADALMYCHG 193
DB  190 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKDFEQRTATITELANALSYCHS 249

QY  194 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
DB  250 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 309

QY  254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAODLISKLLRHNP 313
DB  310 VDLWLSGLVLCYEFVLGKPPFEANTYQETKYRSRVEFTFPDFVTEGARDLISRLKHNPS 369

QY  314 ERUPLAQVSAHPWVRANSRRVLPSPALQS 342
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RESULT 12
US-09-949-016-10461
; Sequence 10461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10461
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10461

Query Match      58.5%; Score 1057.5; DB 4; Length 488;
Best Local Similarity 63.2%; Pred. No. 3.3e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY  22 STLPQVLR-----KEPVTSPALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
DB  167 TSPVHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 214

QY  74 IDDFEIGRPLGKGFQNVYLAREKKSHFIVALKVLFKSKQIEKEGVHQLRRRETEIOAHILH 133
DB  215 LEDFEIGRPLGKGFQNVYLAREKQSKFILALKVLFKAQLEKAGVHQLRRRETEIOASHLR 274

QY  134 HPNILRLYNYFYDRIIRYILLEYAPRGELYKELQKSCTFDEQRTATIMBELADALMYCHG 193
DB  275 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKDFEQRTATITELANALSYCHS 334

QY  194 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
DB  335 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 394

QY  254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAODLISKLLRHNP 313
DB  395 VDLWLSGLVLCYEFVLGKPPFEANTYQETKYRSRVEFTFPDFVTEGARDLISRLKHNPS 454

Query Match      58.5%; Score 1057.5; DB 4; Length 488;
Best Local Similarity 63.2%; Pred. No. 3.3e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY  22 STLPQVLR-----KEPVTSPALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
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DB  167 TSPVHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 214
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QY  134 HPNILRLYNYFYDRIIRYILLEYAPRGELYKELQKSCTFDEQRTATIMBELADALMYCHG 193
DB  275 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKDFEQRTATITELANALSYCHS 334
QY  194 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
DB  335 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 394
QY  254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAODLISKLLRHNP 313
DB  395 VDLWLSGLVLCYEFVLGKPPFEANTYQETKYRSRVEFTFPDFVTEGARDLISRLKHNPS 454
QY  314 ERUPLAQVSAHPWVRANSRRVLPSPALQS 342
DB  455 QRPMLREVLEHPWITANSKK---PSNCQN 480

RESULT 13
US-09-949-016-10462
; Sequence 10462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10462
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10462

Query Match      58.5%; Score 1057.5; DB 4; Length 488;
Best Local Similarity 63.2%; Pred. No. 3.3e-99;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY  22 STLPQVLR-----KEPVTSPALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
DB  167 TSPVHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 214

QY  74 IDDFEIGRPLGKGFQNVYLAREKKSHFIVALKVLFKSKQIEKEGVHQLRRRETEIOAHILH 133
DB  215 LEDFEIGRPLGKGFQNVYLAREKQSKFILALKVLFKAQLEKAGVHQLRRRETEIOASHLR 274

QY  134 HPNILRLYNYFYDRIIRYILLEYAPRGELYKELQKSCTFDEQRTATIMBELADALMYCHG 193
DB  275 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKDFEQRTATITELANALSYCHS 334

QY  194 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
DB  335 KKVHREDIKPENLLGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 394

QY  254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAODLISKLLRHNP 313
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Job time : 41.7617 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:47:43 ; Search time 66.3132 Seconds
(without alignments)
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Title: US-10-734-126-3

Perfect score: 1809

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%

Maximum Match 100%

Listing first 65000 summaries

Database :

Published Applications AA:
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1809	100.0	344	9 US-09-012-135A-3	Sequence 3, Appli
2	1809	100.0	344	11 US-09-784-332-3	Sequence 3, Appli
3	1809	100.0	344	14 US-10-060-065-13	Sequence 13, Appli
4	1809	100.0	344	14 US-10-059-585-34	Sequence 34, Appli
5	1809	100.0	344	14 US-10-171-311-214	Sequence 214, Appli
6	1809	100.0	344	15 US-10-295-027-203	Sequence 203, Appli
7	1809	100.0	344	15 US-10-173-999-101	Sequence 101, Appli
8	1809	100.0	344	15 US-10-188-832-93	Sequence 93, Appli
9	1809	100.0	344	16 US-10-734-126-3	Sequence 3, Appli
10	1797.5	99.4	347	9 US-09-974-298-136	Sequence 136, Appli
11	1520.5	84.1	343	15 US-10-429-849-4	Sequence 4, Appli

12	1181	65.3	355	15	US-10-092-900A-14	Sequence 14, Appli
13	1124	62.1	320	15	US-10-403-571-98	Sequence 98, Appli
14	1057.5	58.5	322	16	US-10-664-421-125	Sequence 125, Appli
15	1057.5	58.5	403	9	US-09-012-135A-4	Sequence 4, Appli
16	1057.5	58.5	403	11	US-09-784-332-4	Sequence 4, Appli
17	1057.5	58.5	403	14	US-10-060-065-12	Sequence 12, Appli
18	1057.5	58.5	403	14	US-10-059-585-33	Sequence 33, Appli
19	1057.5	58.5	403	14	US-10-209-324-2	Sequence 2, Appli
20	1057.5	58.5	403	15	US-10-295-027-1206	Sequence 1206, Appli
21	1057.5	58.5	403	15	US-10-087-684-47	Sequence 47, Appli
22	1057.5	58.5	403	15	US-10-087-684-48	Sequence 48, Appli
23	1057.5	58.5	403	15	US-10-087-684-49	Sequence 49, Appli
24	1057.5	58.5	403	15	US-10-218-779-47	Sequence 47, Appli
25	1057.5	58.5	403	15	US-10-218-779-48	Sequence 48, Appli
26	1057.5	58.5	403	15	US-10-218-779-49	Sequence 49, Appli
27	1057.5	58.5	403	15	US-10-188-832-35	Sequence 35, Appli
28	1057.5	58.5	403	16	US-10-751-736-65	Sequence 65, Appli
29	1057.5	58.5	403	16	US-10-734-126-4	Sequence 4, Appli
30	1057.5	58.5	403	17	US-10-781-581-187	Sequence 187, Appli
31	1057.5	58.5	420	15	US-10-264-049-3090	Sequence 3090, Appli
32	1050.5	58.1	403	14	US-10-026-021-7	Sequence 7, Appli
33	1050.5	58.1	403	15	US-10-087-684-50	Sequence 50, Appli
34	1050.5	58.1	403	15	US-10-218-779-50	Sequence 50, Appli
35	1045.5	57.8	402	15	US-10-087-684-51	Sequence 51, Appli
36	1045.5	57.8	402	15	US-10-218-779-51	Sequence 51, Appli
37	966	53.4	403	15	US-10-087-684-14	Sequence 14, Appli
38	966	53.4	403	15	US-10-218-779-14	Sequence 14, Appli
39	940	52.0	294	15	US-10-389-566-1246	Sequence 1246, Appli
40	937	51.8	294	15	US-10-389-566-1246	Sequence 1246, Appli
41	934.5	51.7	295	15	US-10-389-566-645	Sequence 645, Appli
42	933.5	51.6	298	15	US-10-389-566-644	Sequence 644, Appli
43	921.5	50.9	282	15	US-10-389-566-1240	Sequence 1240, Appli
44	918	50.7	368	15	US-10-389-566-382	Sequence 382, Appli
45	917.5	50.7	418	15	US-10-389-566-819	Sequence 819, Appli
46	916.5	50.7	320	16	US-10-437-963-133574	Sequence 133574, Appli
47	909	50.2	307	15	US-10-424-599-274736	Sequence 274736, Appli
48	908	50.2	298	15	US-10-389-566-550	Sequence 550, Appli
49	906	50.1	432	15	US-10-389-566-2420	Sequence 2420, Appli

ALIGNMENTS

RESULT 1
US-09-012-135A-3
; Sequence 3, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268

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/ FILING DATE: January 9, 1998
/ APPLICATION NUMBER: 08/755,728
/ FILING DATE: No. US20020081578A1ember 25, 1996
/ APPLICATION NUMBER: 60/023,943
/ FILING DATE: August 14, 1996
/ APPLICATION NUMBER: 60/008,809
/ FILING DATE: December 18, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 231/282
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 344 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-09-012-135A-3

Query Match 100.0%; Score 1809; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQRLVKKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVEH 120
DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVEH 120
QY 121 QLRRETEIOAHLHPNLRILNYFYDRRRILYILEYAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETEIOAHLHPNLRILNYFYDRRRILYILEYAPRGELYKELQKCTFDEQRTATI 180
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DB 181 MEELADALMYCHGKVKVTHRDIPENLLGLKGELKIADFGWSVHAPSLRRKTCMGTLDYL 240
QY 241 PPMIEGRMHNEKVLDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
DB 241 PPMIEGRMHNEKVLDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
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DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
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RESULT 2

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US-09-784-332-3
/ Sequence 3, Application US/09784332
/ Publication No. US2005002938A1
/ GENERAL INFORMATION:
/ APPLICANT: Plowman, Gregory
/ Mossie, Kevin
/ TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/784,332
/ FILING DATE: 16-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/283,011
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 09/012,135
/ FILING DATE: January 22, 1998
/ APPLICATION NUMBER: 08/755,728
/ FILING DATE: November 25, 1996
/ APPLICATION NUMBER: 60/023,943
/ FILING DATE: August 14, 1996
/ APPLICATION NUMBER: 60/008,809
/ FILING DATE: December 18, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 231/282
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 344 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
/ US-09-784-332-3

Query Match 100.0%; Score 1809; DB 11; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 QLRRETEIOAHLHPNLRILNYFYDRRRILYILEYAPRGELYKELQKCTFDEQRTATI 180
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DB 181 MEELADALMYCHGKVKVTHRDIPENLLGLKGELKIADFGWSVHAPSLRRKTCMGTLDYL 240
QY 241 PPMIEGRMHNEKVLDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
DB 241 PPMIEGRMHNEKVLDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
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RESULT 3

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US-10-060-065-13
/ Sequence 13, Application US/10060065
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Publication No. US20030017480A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Kaoru Otsuka
APPLICANT: Jun-ichi Yamamoto
APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Keiichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Jun-ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT FILING DATE: 2002-01-29
PRIORITY APPLICATION NUMBER: PCT/JP00/05061
PRIORITY FILING DATE: 2000-07-28
PRIORITY APPLICATION NUMBER: US 60/159,590
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: US 60/183,322
PRIORITY FILING DATE: 2000-02-17
PRIORITY APPLICATION NUMBER: JP 11-248036
PRIORITY FILING DATE: 1999-07-29
PRIORITY APPLICATION NUMBER: JP 2000-118776
PRIORITY FILING DATE: 2000-01-11
PRIORITY APPLICATION NUMBER: JP 2000-183767
PRIORITY FILING DATE: 2000-05-02
PRIORITY APPLICATION NUMBER: JP 2000-241899
PRIORITY FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-065-13

Query Match 100.0%; Score 1809; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVTSPALVLMRSNNVQPTAAPGQKWMEN 60
QY 61 SSGTDPILTRHFTDIDDFEIGRPLGKGFNGVYLAREKKS HFI VALKVL FKSQIEKEGVEH 120
DB 61 SSGTDPILTRHFTDIDDFEIGRPLGKGFNGVYLAREKKS HFI VALKVL FKSQIEKEGVEH 120
QY 121 QLRRREIEIOAHLHPNLRILYNYFYDRRRILYLEVAPRGELKELKSCCTFDEQRTATI 180
DB 121 QLRRREIEIOAHLHPNLRILYNYFYDRRRILYLEVAPRGELKELKSCCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVTHRDIPENLLGLKGLKLTADFCWSVHAPSLRRTKTCGTLDDYL 240
DB 181 MEELADALMYCHGKKVTHRDIPENLLGLKGLKLTADFCWSVHAPSLRRTKTCGTLDDYL 240
QY 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRI VKVDL KFPASVPTGA 300
DB 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRI VKVDL KFPASVPTGA 300
QY 301 QDLISKLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
DB 301 QDLISKLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344

RESULT 4
US-10-059-585-34

Sequence 34, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsuji
APPLICANT: Funahashi, Shin-ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-ichi
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIORITY APPLICATION NUMBER: PCT/JP00/05060
PRIORITY FILING DATE: 2000-07-28
PRIORITY APPLICATION NUMBER: US 60/183,322
PRIORITY FILING DATE: 2000-02-17
PRIORITY APPLICATION NUMBER: US 60/159,590
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: JP 2000-118776
PRIORITY FILING DATE: 2000-01-11
PRIORITY APPLICATION NUMBER: JP 2000-183767
PRIORITY FILING DATE: 2000-05-02
PRIORITY APPLICATION NUMBER: JP 11-248036
PRIORITY FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-10-059-585-34

Query Match 100.0%; Score 1809; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVTSPALVLMRSNNVQPTAAPGQKWMEN 60
DB 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVTSPALVLMRSNNVQPTAAPGQKWMEN 60
QY 61 SSGTDPILTRHFTDIDDFEIGRPLGKGFNGVYLAREKKS HFI VALKVL FKSQIEKEGVEH 120
DB 61 SSGTDPILTRHFTDIDDFEIGRPLGKGFNGVYLAREKKS HFI VALKVL FKSQIEKEGVEH 120
QY 121 QLRRREIEIOAHLHPNLRILYNYFYDRRRILYLEVAPRGELKELKSCCTFDEQRTATI 180
DB 121 QLRRREIEIOAHLHPNLRILYNYFYDRRRILYLEVAPRGELKELKSCCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVTHRDIPENLLGLKGLKLTADFCWSVHAPSLRRTKTCGTLDDYL 240
DB 181 MEELADALMYCHGKKVTHRDIPENLLGLKGLKLTADFCWSVHAPSLRRTKTCGTLDDYL 240
QY 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRI VKVDL KFPASVPTGA 300
DB 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRI VKVDL KFPASVPTGA 300
QY 301 QDLISKLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
DB 301 QDLISKLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344

RESULT 5
US-10-171-311-214

```
; Sequence 214, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; TYPE: PRT
; LENGTH: 344
; ORGANISM: Homo sapiens
; US-10-171-311-214

Query Match      100.0%; Score 1809; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 7,6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWYGRQTAPSGSLTPQRLRKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWYGRQTAPSGSLTPQRLRKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGV 120
DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGV 120
QY 121 QLRRETEIQAHLLHPNLRNYFYDRRRILYILEYAPRGELYKELQKCTPDEQRTATI 180
DB 121 QLRRETEIQAHLLHPNLRNYFYDRRRILYILEYAPRGELYKELQKCTPDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGELKIADFGWSVHAPSLRRKTCGTL 240
DB 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGELKIADFGWSVHAPSLRRKTCGTL 240
QY 241 PPMIEGRMHNEKVLDWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKPASVPTGA 300
DB 241 PPMIEGRMHNEKVLDWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 6
US-10-295-027-203
; Sequence 203, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevesi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
```

```
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-203

Query Match      100.0%; Score 1809; DB 15; Length 344;
Best Local Similarity 100.0%; Pred. No. 7,6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWYGRQTAPSGSLTPQRLRKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWYGRQTAPSGSLTPQRLRKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGV 120
DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGV 120
QY 121 QLRRETEIQAHLLHPNLRNYFYDRRRILYILEYAPRGELYKELQKCTPDEQRTATI 180
DB 121 QLRRETEIQAHLLHPNLRNYFYDRRRILYILEYAPRGELYKELQKCTPDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGELKIADFGWSVHAPSLRRKTCGTL 240
DB 181 MEELADALMYCHGKVKVTHRDIKPENLLGLKGELKIADFGWSVHAPSLRRKTCGTL 240
QY 241 PPMIEGRMHNEKVLDWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKPASVPTGA 300
DB 241 PPMIEGRMHNEKVLDWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 7
US-10-173-999-101
; Sequence 101, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
```

;; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
;; TITLE OF INVENTION: Cancer
;; FILE REFERENCE: 018501-00242005
;; CURRENT APPLICATION NUMBER: US/10/173,999
;; CURRENT FILING DATE: 2002-06-17
;; APPLICATION NUMBER: US 60/299,234
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: US 60/315,287
;; PRIOR FILING DATE: 2001-08-27
;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/372,246
;; PRIOR FILING DATE: 2001-04-12
;; NUMBER OF SEQ ID NOS: 163
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 101
;; LENGTH: 344
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-173-999-101

Query Match 100.0%; Score 1809; DB 15; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQKENSYPYGRQGTAPSGSLTLPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
Db 1 MAQKENSYPYGRQGTAPSGSLTLPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60

Qy 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
Db 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120

Qy 121 QLARETEIOAHLHPNLRILYNYFYDRRRYLLILEVAPRGELKELQKCTFEQRTATI 180
Db 121 QLARETEIOAHLHPNLRILYNYFYDRRRYLLILEVAPRGELKELQKCTFEQRTATI 180

Qy 181 MEELADALMYCHGKVKVHRDIKPENLLGLKGLKIADFGWSVHAPSRLRKTTCGTLTDL 240
Db 181 MEELADALMYCHGKVKVHRDIKPENLLGLKGLKIADFGWSVHAPSRLRKTTCGTLTDL 240

Qy 241 PPMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIKVDLKFPAASVPTGA 300
Db 241 PPMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIKVDLKFPAASVPTGA 300

Qy 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
Db 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 8
US-10-188-832-93
; Sequence 93, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: MacK, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-00233005
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13

;; PRIOR APPLICATION NUMBER: US 60/372,246
;; PRIOR FILING DATE: 2002-04-12
;; NUMBER OF SEQ ID NOS: 207
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 93
;; LENGTH: 344
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-188-832-93

Query Match 100.0%; Score 1809; DB 15; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQKENSYPYGRQGTAPSGSLTLPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
Db 1 MAQKENSYPYGRQGTAPSGSLTLPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60

Qy 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
Db 61 SSGTDPDLTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120

Qy 121 QLARETEIOAHLHPNLRILYNYFYDRRRYLLILEVAPRGELKELQKCTFEQRTATI 180
Db 121 QLARETEIOAHLHPNLRILYNYFYDRRRYLLILEVAPRGELKELQKCTFEQRTATI 180

Qy 181 MEELADALMYCHGKVKVHRDIKPENLLGLKGLKIADFGWSVHAPSRLRKTTCGTLTDL 240
Db 181 MEELADALMYCHGKVKVHRDIKPENLLGLKGLKIADFGWSVHAPSRLRKTTCGTLTDL 240

Qy 241 PPMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIKVDLKFPAASVPTGA 300
Db 241 PPMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIKVDLKFPAASVPTGA 300

Qy 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
Db 301 QDLISKLLRHPNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 9
US-10-734-126-3
; Sequence 3, Application US/10734126
; Publication No. US20040265852A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,126
; FILING DATE: 15-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,332
; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 09/283,011
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/012,135

```
;
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: November 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-734-126-3

Query Match      100.0%; Score 1809; DB 16; Length 344;
Best Local Similarity 100.0%; Pred. No. 7.6e-140;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQRLVKKEPTVPSALVLMRSNVQPTAAPGQKVMEN 60
Db 1 MAQKENSYPWPYGRQTAPSGSLTLPQRLVKKEPTVPSALVLMRSNVQPTAAPGQKVMEN 60

QY 61 SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVGH 120
Db 61 SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVGH 120

QY 121 QLRRREIEQAHLPNHLNLYNYFYDRRIYLLIYAPRGELYKELQKCTFDEQRTAT 180
Db 121 QLRRREIEQAHLPNHLNLYNYFYDRRIYLLIYAPRGELYKELQKCTFDEQRTAT 180

QY 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLARKKTCGTL 240
Db 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLARKKTCGTL 240

QY 241 PPMEIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYVKVLDKFPASVPTGA 300
Db 241 PPMEIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYVKVLDKFPASVPTGA 300

QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
Db 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344

RESULT 10
US-09-974-298-136
; Sequence 136, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 136
; LENGTH: 347
; TYPE: PRT
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;
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 002940CD1
US-09-974-298-136

Query Match      99.4%; Score 1797.5; DB 9; Length 347;
Best Local Similarity 99.1%; Pred. No. 6.7e-139;
Matches 344; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQRLVKKEPTVPSALVLMRSNVQPTAAPGQKVMEN 60
Db 1 MAQKENSYPWPYGRQTAPSGSLTLPQRLVKKEPTVPSALVLMRSNVQPTAAPGQKVMEN 60

QY 61 SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVGH 120
Db 61 SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEGVGH 120

QY 121 QLRRREIEQAHLPNHLNLYNYFYDRRIYLLIYAPRGELYKELQKCTFDEQRTAT 179
Db 121 QLRRREIEQAHLPNHLNLYNYFYDRRIYLLIYAPRGELYKELQKCTFDEQRTAT 180

QY 180 --IMEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLARKKTCGTL 237
Db 181 RAMEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLARKKTCGTL 240

QY 238 DYLPPMEIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYVKVLDKFPASV 297
Db 241 DYLPPMEIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYVKVLDKFPASV 300

QY 298 TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
Db 301 TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSA 347

RESULT 11
US-10-429-849-4
; Sequence 4, Application US/10429849
; Publication No. US20040029157A1
; GENERAL INFORMATION:
; APPLICANT: TATSUKA, MASAAKI
; APPLICANT: TERADA, YASUHIKO
; TITLE OF INVENTION: CELL CYCLE-REGULATING PROTEINS
; FILE REFERENCE: 050499/0102
; CURRENT APPLICATION NUMBER: US/10/429,849
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US/09/485,534
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/JP98/03641
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 235371/1997
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-429-849-4

Query Match      84.1%; Score 1520.5; DB 15; Length 343;
Best Local Similarity 84.5%; Pred. No. 3.2e-116;
Matches 290; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQRLVKKEPTVPSALVLMRSNVQPTAAPGQKVMEN 60
Db 1 MAQKENVYPWPYSGSKTSQSGSLNTLPQRLVKKEPAVTPAQLMNRNSQSTAVPGQLTEN 60

QY 61 SSGTP---DILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEG 117
Db 61 KGATALQGSQSRQPFIDNFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIKEG 120

QY 118 VEHQLRREIEQAHLPNHLNLYNYFYDRRIYLLIYAPRGELYKELQKCTFDEQRT 177
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Query Match 58.5%; Score 1057.5; DB 14; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPRQVLR-----KEPVTPSALVLMRSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVHQHRRREIEIOAHLH 133
Db 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKLVLFKAQLEKAGVEHQHRRREIEIOASHLR 189

QY 134 HNNILRLNYFYDRIIYILEYAPRGELYKELQKSCCTDEORTATIMEELADALMYCHG 193
Db 190 HNNILRLYGYFHDATRVYLILEYAPLGTVTYRELOKLSKFEDEORTATYITELANALSYCHS 249

QY 194 KKVHHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253
Db 250 KKVHHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEMIEGRMHDEK 309

QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
Db 310 VDLWSLGVLCYELVKGKPPFEANTYQETVKRISRVEFTFPDFVTEGARDLISLLKHNP 369

QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLEHPWITANSSK---PSNCQN 395

RESULT 18
US-10-059-585-33
; Sequence 33, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayaashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-33

Query Match 58.5%; Score 1057.5; DB 14; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPRQVLR-----KEPVTPSALVLMRSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVHQHRRREIEIOAHLH 133
Db 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKLVLFKAQLEKAGVEHQHRRREIEIOASHLR 189

QY 134 HNNILRLNYFYDRIIYILEYAPRGELYKELQKSCCTDEORTATIMEELADALMYCHG 193
Db 190 HNNILRLYGYFHDATRVYLILEYAPLGTVTYRELOKLSKFEDEORTATYITELANALSYCHS 249

QY 194 KKVHHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253
Db 250 KKVHHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEMIEGRMHDEK 309

QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
Db 310 VDLWSLGVLCYELVKGKPPFEANTYQETVKRISRVEFTFPDFVTEGARDLISLLKHNP 369

QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLEHPWITANSSK---PSNCQN 395

RESULT 19
US-10-209-324-2
; Sequence 2, Application US/10209324
; Publication No. US20030108910A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
; APPLICANT: TOLAND, Amanda E.
; APPLICANT: BALMAIN, Allan
; TITLE OF INVENTION: STR15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
; FILE REFERENCE: UCSF1120-2
; CURRENT APPLICATION NUMBER: US/10/209,324
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US 60/334,146
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/308,911
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: Xaa is Ile or Phe
US-10-209-324-2

Query Match 58.5%; Score 1057.5; DB 14; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPRQVLR-----KEPVTPSALVLMRSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVHQHRRREIEIOAHLH 133
Db 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKLVLFKAQLEKAGVEHQHRRREIEIOASHLR 189

QY 134 HNNILRLNYFYDRIIYILEYAPRGELYKELQKSCCTDEORTATIMEELADALMYCHG 193
Db 190 HNNILRLYGYFHDATRVYLILEYAPLGTVTYRELOKLSKFEDEORTATYITELANALSYCHS 249

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QY 194 KKVHRIKPEENLIGLKGELKIADFGWSVHAPSLRRKTCMGTLDVLPPEMIEGRMHNEK 253
Db 250 KKVHRIKPEENLIGLKGELKIADFGWSVHAPSLRRKTCMGTLDVLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSLGVLCYELVGNKPPPEANTYQETKYRISRVFTFDFVTEGARDLISRLKHNS 369
QY 314 ERPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLHPWITANSK---PSNCQN 395

RESULT 20
US-10-295-027-1206
; Sequence 1206, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1206
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1206

Query Match 58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPQVLR-----KEPVTSAVLMSRSNVQPTAAPGQKVMNSGCTPDILTRHFT 73
Db 82 TSVPHVPSRLNNTQKSKQPL-PSA-----PENNPEELASKQKNBSKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKSOIEKEGVHQLRREIEIQALH 133
Db 130 LEDFEIGRPLGKGFNGVYLAREKSKFILALKVLPKAOLEKAGVHQLRREIEIQSHLR 189
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QY 134 HPNILRYNYFDRRIYILILEYAPRGELYKELQKSCCTFDEORTATIMEELADALMYCHG 193
Db 190 HPNILRYGYFHDATRVYILEYAPLGTVYRELQKLSKFDEORTATYITELANALSYCHS 249
QY 194 KKVHRIKPEENLIGLKGELKIADFGWSVHAPSLRRKTCMGTLDVLPPEMIEGRMHNEK 253
Db 250 KKVHRIKPEENLIGLKGELKIADFGWSVHAPSLRRKTCMGTLDVLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSLGVLCYELVGNKPPPEANTYQETKYRISRVFTFDFVTEGARDLISRLKHNS 369
QY 314 ERPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 370 QRPMLREVLHPWITANSK---PSNCQN 395

RESULT 21
US-10-087-684-47
; Sequence 47, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Fadigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Baha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-47

Query Match 58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
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Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLPRVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMENSGTDPDLTRHFT 73
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
82 TSVPHVPVSRPLNNTQKSKQL-PSA-----PENNPBEELASKQKNESKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHILH 133
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
130 LEDFEIGRPLGKGFNGVYLAREKSKFILAUKVLFKAQLEKAGVHQLRREIEIOHSLR 189
QY 134 HPNILRLNYFYDRRIYILILEYAPRGELYKELOKSCTFDEQRTATIMEELADALMYCHG 193
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
190 HPNILRLNYGYFHDATRVYILLEYAPLGTVYVRELQKLSKFDEQRTATYITELANALSYCHS 249
QY 194 KVIHRDIKPENLLIGKELKTADFGWSVHAPSLARKTCMGTDLVLPPEMIEGRMHNEK 253
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
250 KRVIHRDIKPENLLIGSAGELKIADFGWSVHAPSSRRTTLCGTDLVLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
310 VDLWSLGVLCYELFVKGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLISRLKHNP 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 22
US-10-087-684-48
; Sequence 48, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Baha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; PRIOR FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220

; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 48
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-48

Query Match 58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLPRVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMENSGTDPDLTRHFT 73
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
82 TSVPHVPVSRPLNNTQKSKQL-PSA-----PENNPBEELASKQKNESKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHILH 133
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
130 LEDFEIGRPLGKGFNGVYLAREKSKFILAUKVLFKAQLEKAGVHQLRREIEIOHSLR 189
QY 134 HPNILRLNYFYDRRIYILILEYAPRGELYKELOKSCTFDEQRTATIMEELADALMYCHG 193
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
190 HPNILRLNYGYFHDATRVYILLEYAPLGTVYVRELQKLSKFDEQRTATYITELANALSYCHS 249
QY 194 KVIHRDIKPENLLIGKELKTADFGWSVHAPSLARKTCMGTDLVLPPEMIEGRMHNEK 253
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
250 KRVIHRDIKPENLLIGSAGELKIADFGWSVHAPSSRRTTLCGTDLVLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
310 VDLWSLGVLCYELFVKGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLISRLKHNP 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 23
US-10-087-684-49
; Sequence 49, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Baha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
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; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curated version 0.1
; SEQ ID NO 49
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-684-49

Query Match      58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPQVLR-----KEPVTPSALVLMRSNVQPTAAPGQKWMENSGTDPILTRHFT 73
DB 82 TSVPHVPSRPLNNTQKSKQPL-PSA-----PENNPEELASKQNESSKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFNGVYLAREKQKSFILALKVLFKAQLEKAGVHQHQLRREIEIOSHLR 189
QY 134 HPNILRLNYFYDRRIYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193
DB 190 HPNILRLNYGYFHDAIVYLLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 249
QY 194 KKVHRIKIPENLLGLKGLKELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVHRIKIPENLLGLKGLKELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKPASVPTCAODLISKLLRHNS 313
DB 310 VDLWSGLVLCYELFVGKPPFEANTYQETKYRISRVEFTFPDFVTEGARDLISRLLKHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 24
US-10-218-779-47
; Sequence 47, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
```

```
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 47
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-47

Query Match      58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPQVLR-----KEPVTPSALVLMRSNVQPTAAPGQKWMENSGTDPILTRHFT 73
DB 82 TSVPHVPSRPLNNTQKSKQPL-PSA-----PENNPEELASKQNESSKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFNGVYLAREKQKSFILALKVLFKAQLEKAGVHQHQLRREIEIOSHLR 189
QY 134 HPNILRLNYFYDRRIYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193
DB 190 HPNILRLNYGYFHDAIVYLLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 249
QY 194 KKVHRIKIPENLLGLKGLKELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVHRIKIPENLLGLKGLKELKIADFGWSVHAPSLRRKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKPASVPTCAODLISKLLRHNS 313
DB 310 VDLWSGLVLCYELFVGKPPFEANTYQETKYRISRVEFTFPDFVTEGARDLISRLLKHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 25
US-10-218-779-48
; Sequence 48, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
```



```
RESULT 27
US-10-188-832-35
; Sequence 35, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-35

Query Match      58.5%; Score 1057.5; DB 15; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQVR-----KEPVTSALVMSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSVPHVPSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDPFGRLGKGFNGVYLAREKSHFIVALKVLPKSOIEKGVHQLREIEIOAHLH 133
Db 130 LEDFEGRLGKGFNGVYLAREKSHFIVALKVLPKSOIEKGVHQLREIEIOAHLH 189

QY 134 HPNLRILYFYDRLRYLILEYAPRGELKQKCTFDEORTATIMEELADALMYCHG 193
Db 190 HPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEORTATITELANALSCHS 249

QY 194 KKVIRHDIKPENLLGLKGBELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMNEK 253
Db 250 KKVIRHDIKPENLLGLKGBELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMDEK 309

QY 254 VDLWCIGVLCYELLGNPPESASHNETYRIKVDLKPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSGLVLCYELGKPPPEANTYQTYKRISRVEFTFPDFTVEGARDLISRLKHNPS 369

QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db 370 QRPMLREVLHPWITANSSK---PSNCQN 395

RESULT 28
US-10-751-736-65
; Sequence 65, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
```

```
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-751-736-65

Query Match      58.5%; Score 1057.5; DB 16; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQVR-----KEPVTSALVMSRNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSVPHVPSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDPFGRLGKGFNGVYLAREKSHFIVALKVLPKSOIEKGVHQLREIEIOAHLH 133
Db 130 LEDFEGRLGKGFNGVYLAREKSHFIVALKVLPKSOIEKGVHQLREIEIOAHLH 189

QY 134 HPNLRILYFYDRLRYLILEYAPRGELKQKCTFDEORTATIMEELADALMYCHG 193
Db 190 HPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEORTATITELANALSCHS 249

QY 194 KKVIRHDIKPENLLGLKGBELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMNEK 253
Db 250 KKVIRHDIKPENLLGLKGBELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEMIEGRMDEK 309

QY 254 VDLWCIGVLCYELLGNPPESASHNETYRIKVDLKPASVPTGAQDLISKLLRHNS 313
Db 310 VDLWSGLVLCYELGKPPPEANTYQTYKRISRVEFTFPDFTVEGARDLISRLKHNPS 369

QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db 370 QRPMLREVLHPWITANSSK---PSNCQN 395

RESULT 29
US-10-734-126-4
; Sequence 4, Application US/10734126
; Publication No. US20040265852A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/734,126
; FILING DATE: 15-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US/09/784,332
```

; FILING DATE: 16-Feb-2001
; APPLICATION NUMBER: 09/283,011
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: November 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-734-126-4

Query Match 58.5%; Score 1057.5; DB 16; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLQQRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMNSGSGTDPDLTRHFT 73
DB 82 TSVPHVSRPLNNTQSKQPL-PSA----PENNPEELASKQKNEESKK-----ROWA 129
QY 74 IDDFEIGRLGKGFNGVYLAREKSHFVALKVLFKSQIEKEGVHQLRREIEIOAHLLH 133
DB 130 LEDFEIGRLGKGFNGVYLAREKSHFVALKVLFKSQIEKEGVHQLRREIEIOAHLLH 189
QY 134 HPNILRLYNYFYDRRIYILLEYAPRGELYKELQKSCFDEQRTATIMEELADALMYCHG 193
DB 190 HPNILRLYGYFHDATRVYILLEYAPLGTVYRELQKSKFDEQRTATYITELANALSYCHS 249
QY 194 KKVIRHDIKPENLLGLGKELKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVIRHDIKPENLLGLGKELKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPTCAQDLISKLLRHNS 313
DB 310 VDLWSLGLVCYELFLVGKPPFEANTYQETKYKRISRVETFPDFVTEGARDLISRLLKHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 30
US-10-781-581-187
; Sequence 187, Application US/10781581
; Publication No. US20050019746A1
; GENERAL INFORMATION:
; APPLICANT: Eirx Therapeutics Ltd.
; APPLICANT: Seery, Liam
; APPLICANT: Hayes, Ian
; APPLICANT: Murphy, Finbarr
; TITLE OF INVENTION: Apoptosis-Related Kinase/GPCR
; FILE REFERENCE: 8912/2015
; CURRENT APPLICATION NUMBER: US/10/781,581
; CURRENT FILING DATE: 2004-02-18

; PRIOR APPLICATION NUMBER: US 10/764,238
; PRIOR FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/457,533
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: UK 0301566.6
; PRIOR FILING DATE: 2003-01-23
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-581-187
Query Match 58.5%; Score 1057.5; DB 17; Length 403;
Best Local Similarity 63.2%; Pred. No. 3.3e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLQQRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMNSGSGTDPDLTRHFT 73
DB 82 TSVPHVSRPLNNTQSKQPL-PSA----PENNPEELASKQKNEESKK-----ROWA 129
QY 74 IDDFEIGRLGKGFNGVYLAREKSHFVALKVLFKSQIEKEGVHQLRREIEIOAHLLH 133
DB 130 LEDFEIGRLGKGFNGVYLAREKSHFVALKVLFKSQIEKEGVHQLRREIEIOAHLLH 189
QY 134 HPNILRLYNYFYDRRIYILLEYAPRGELYKELQKSCFDEQRTATIMEELADALMYCHG 193
DB 190 HPNILRLYGYFHDATRVYILLEYAPLGTVYRELQKSKFDEQRTATYITELANALSYCHS 249
QY 194 KKVIRHDIKPENLLGLGKELKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVIRHDIKPENLLGLGKELKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPTCAQDLISKLLRHNS 313
DB 310 VDLWSLGLVCYELFLVGKPPFEANTYQETKYKRISRVETFPDFVTEGARDLISRLLKHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 31
US-10-264-049-3090
; Sequence 3090, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3090
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-3090
Query Match 58.5%; Score 1057.5; DB 15; Length 420;
Best Local Similarity 63.2%; Pred. No. 3.5e-78;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLQQRVLR-----KEPVTPSALVMSRSNVQPTAAPGQKVMNSGSGTDPDLTRHFT 73
DB 99 TSVPHVSRPLNNTQSKQPL-PSA----PENNPEELASKQKNEESKK-----ROWA 146

US-10-087-684-51

Query Match 57.8%; Score 1045.5; DB 15; Length 402;
Best Local Similarity 54.8%; Pred. No. 3.2e-77;
Matches 216; Conservative 44; Mismatches 75; Indels 59; Gaps 8;

Qy 4 KENSYPWPGYGRQTAPSG-----LSTLP-----ORVL-----RKEPVTTPSA 38
Db 5 KENCISGPV-KATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCPSNSSQRVPLQAOK 63
Qy 39 LV-----LMSRSNVQPTAAPGQKWMENSSGTPD-----ILTRHF----- 72
Db 64 LVSSHKPVQKQKQLQATSVPHPSRPLNNTQKSKPLFSLKILLRNWHQNRKMNQ 123
Qy 73 -----TDDFFIGRPLGKGFNVYLAREKSHFIVALKVLFKQIEKEGVEHOLRREIEI 128
Db 124 KEAVALDEDFEIGRPLGKGFNVYLAREKSKETILALKVLFKAQLEKAGVEHQLRREVEI 183
Qy 129 QAHLHPNILRLNYFYDRRIYLIILEYAPRGELYKELQKSCFTDEORTATIMEELADAL 188
Db 184 QSHLRHPNILRLNYFYDFHATRVYLIILEYAPLGTVYRELQKLSKFDEORTANLYNRANAL 243
Qy 189 MYCHGKKVIHRDIKPNENLLGLKGLKIADFGSVHAPSRRRTKTCGTLDYLPPEMIEGR 248
Db 244 SYCHSKRVIHRDIKPNENLLGSAGELKIADFGSVHAPSRRRTLCGTLDYLPPEMIEGR 303
Qy 249 MHNEKVDLWCIGVLCYELLVGNPPFSASHNETYRIRIVKVDLKFPPASVPTGAQDLISKLL 308
Db 304 MHDEKVDLWSLGVLCYELVGNPPFEANTYQETIKRISRVFEFTFPDPVTEGARDLISRLL 363
Qy 309 RHPNSELPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 364 KHNPSQRPMLREVLEHPWITANSK---PSNCON 394

RESULT 36

US-10-218-779-51
; Sequence 51, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangoli, Baha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-218-779-51

Query Match 57.8%; Score 1045.5; DB 15; Length 402;
Best Local Similarity 54.8%; Pred. No. 3.2e-77;
Matches 216; Conservative 44; Mismatches 75; Indels 59; Gaps 8;

Qy 4 KENSYPWPGYGRQTAPSG-----LSTLP-----ORVL-----RKEPVTTPSA 38
Db 5 KENCISGPV-KATAPVGGPKRVLVTQOFPQCNPLPVNSGQAQVLCPSNSSQRVPLQAOK 63
Qy 39 LV-----LMSRSNVQPTAAPGQKWMENSSGTPD-----ILTRHF----- 72
Db 64 LVSSHKPVQKQKQLQATSVPHPSRPLNNTQKSKPLFSLKILLRNWHQNRKMNQ 123
Qy 73 -----TDDFFIGRPLGKGFNVYLAREKSHFIVALKVLFKQIEKEGVEHOLRREIEI 128
Db 124 KEAVALDEDFEIGRPLGKGFNVYLAREKSKETILALKVLFKAQLEKAGVEHQLRREVEI 183
Qy 129 QAHLHPNILRLNYFYDRRIYLIILEYAPRGELYKELQKSCFTDEORTATIMEELADAL 188
Db 184 QSHLRHPNILRLNYFYDFHATRVYLIILEYAPLGTVYRELQKLSKFDEORTANLYNRANAL 243
Qy 189 MYCHGKKVIHRDIKPNENLLGLKGLKIADFGSVHAPSRRRTKTCGTLDYLPPEMIEGR 248
Db 244 SYCHSKRVIHRDIKPNENLLGSAGELKIADFGSVHAPSRRRTLCGTLDYLPPEMIEGR 303
Qy 249 MHNEKVDLWCIGVLCYELLVGNPPFSASHNETYRIRIVKVDLKFPPASVPTGAQDLISKLL 308
Db 304 MHDEKVDLWSLGVLCYELVGNPPFEANTYQETIKRISRVFEFTFPDPVTEGARDLISRLL 363
Qy 309 RHPNSELPLAQVSAHPWVRANSRRVLPSPALQS 342
Db 364 KHNPSQRPMLREVLEHPWITANSK---PSNCON 394

RESULT 37

US-10-087-684-14
; Sequence 14, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.

APPLICANT: Zerhusen, Bryan D.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Gangolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-214 CIP
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT FILING DATE: 2003-03-10
PRIOR FILING DATE: 2003-03-10
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 14
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-087-684-14

Query Match 53.4%; Score 966; DB 15; Length 403;
Best Local Similarity 61.8%; Pred. No. 1e-70;
Matches 186; Conservative 41; Mismatches 68; Indels 6; Gaps 2;

QY 45 SNVQPTAAP---GQKWNSSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHF 101
DB 98 SKQSPLSAPENNPEELASKQNEESKKQWALEDLIEIGRPPGKGFNGVYLAREKQSKF 157
QY 102 IVALKVLFSQIEKEGVEHQLRREIEIOAHLHPNLRNYFYDRRRYVILEYAPRGE 161
DB 158 ILALRVLFKAQLEKAGVEHQLRREIEIOAHLHPNLRNYFYDRRRYVILEYTPLET 217
QY 162 LYKELQKSTCFDEORTATIMEELADALMYCHGKVKVTHRDIKPENLLGLKGLKADFGW 221
DB 218 VNTLQKLSKDFDEORTATITELASALSYSCHSKTVIHRDIKPENLLGLSAGELEIANFGW 277
QY 222 SVHAPSLRRTKTCGTLDTLPPMIEGRMNEKVDLWCIGVLYELLVGNPPFESASHNET 281
DB 278 SEHAPSSRRRTTLCGTLDTLPPMIEGRMNEKVDLWLSGLVLCCEFLVGRKPPFANTYQET 337
QY 282 YRRIKVDLKFASVPTGAQDLISKLLRHNPSERLPLAQSHPWVRANSRRVLPSPALQ 341
DB 338 YKRISRVEFTFPDFTVEGARDLLISRLKHPVPSQRPMLREVLEYPWITANSK---PSNCQ 394
QY 342 S 342
DB 395 N 395

RESULT 38
US-10-218-779-14
Sequence 14, Application US/10218779
Publication No. US20040029222A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William
APPLICANT: Alsbrook II, John
APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel

APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-779-14

Query Match 53.4%; Score 966; DB 15; Length 403;
Best Local Similarity 61.8%; Pred. No. 1e-70;
Matches 186; Conservative 41; Mismatches 68; Indels 6; Gaps 2;

QY 45 SNVQPTAAP---GQKWNSSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHF 101
DB 98 SKQSPLSAPENNPEELASKQNEESKKQWALEDLIEIGRPPGKGFNGVYLAREKQSKF 157
QY 102 IVALKVLFSQIEKEGVEHQLRREIEIOAHLHPNLRNYFYDRRRYVILEYAPRGE 161
DB 158 ILALRVLFKAQLEKAGVEHQLRREIEIOAHLHPNLRNYFYDRRRYVILEYTPLET 217
QY 162 LYKELQKSTCFDEORTATIMEELADALMYCHGKVKVTHRDIKPENLLGLKGLKADFGW 221
DB 218 VNTLQKLSKDFDEORTATITELASALSYSCHSKTVIHRDIKPENLLGLSAGELEIANFGW 277
QY 222 SVHAPSLRRTKTCGTLDTLPPMIEGRMNEKVDLWCIGVLYELLVGNPPFESASHNET 281
DB 278 SEHAPSSRRRTTLCGTLDTLPPMIEGRMNEKVDLWLSGLVLCCEFLVGRKPPFANTYQET 337
QY 282 YRRIKVDLKFASVPTGAQDLISKLLRHNPSERLPLAQSHPWVRANSRRVLPSPALQ 341
DB 338 YKRISRVEFTFPDFTVEGARDLLISRLKHPVPSQRPMLREVLEYPWITANSK---PSNCQ 394
QY 342 S 342
DB 395 N 395

RESULT 39
US-10-389-566-1246
Sequence 1246, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:

Db	264	LVKDSQRPLHLKLEHPWIVQNA	287
RESULT 42			
US-10-389-566-644			
; Sequence 644, Application US/10389566			
; Publication No. US20040025202A1			
; GENERAL INFORMATION:			
; APPLICANT: Monsanto Technology, LLC			
; APPLICANT: Laurie, Cathy C			
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants			
; FILE REFERENCE: 38-77(52900)D			
; CURRENT APPLICATION NUMBER: US/10/389,566			
; CURRENT FILING DATE: 2003-03-31			
; PRIOR APPLICATION NUMBER: US 60/365,301			
; PRIOR FILING DATE: 2002-03-15			
; PRIOR APPLICATION NUMBER: US 60/391,786			
; PRIOR FILING DATE: 2002-06-25			
; PRIOR APPLICATION NUMBER: US 60/392,018			
; PRIOR FILING DATE: 2002-06-26			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 644			
; LENGTH: 298			
; TYPE: PRT			
; ORGANISM: Glycine max			
US-10-389-566-644			
Query Match 51.6%; Score 933.5; DB 15; Length 298;			
Best Local Similarity 65.5%; Pred. No. 3.3e-68;			
Matches 173; Conservative 44; Mismatches 44; Indels 3; Gaps 2;			
Qy	70	RHTTDDFEIGPLGKGFNNVLAAREKSHFIVALKVLFKSOIEKEGVEHQLRREIEIQ	129
Db	28	RRWLDFDGLGKPLGKGFHVLAREKTSNHIIVALKVLFKSOIQSQVQLRREIEIQ	87
Qy	130	AHLHPNLRILNYFYDRRIILILEYAPRGELYKELQKCTFDEQRTATIMEELADLM	189
Db	88	SHLRHPHILRLYGYFYDQKRVLLILEYAPKGLYKELQKCYFSERRAATVVASLARALI	147
Qy	190	YCHGKGVHRIKIPENLLILGKELKIADFGWSVHAPSRLRKTMCCTGLDYLPPMIEGRM	249
Db	148	YCHGKGVHRIKIPENLLILGKELKIADFGWSVHTFN-RRRTMCGTGLDYLPPMIEGRM	206
Qy	250	HNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKDLKFPAS--VPTGAODLISKL	307
Db	207	HDASVDIWSLGVLCYFLLGVPPFEAREHSTYRRIIVQDLKFPKPIVSSAKDLISQM	266
Qy	308	LRHNPSEIRPLAQVSAHPWVRANS 331	
Db	267	LVKDSQRPLHLKLEHPWIVQNA 290	
RESULT 43			
US-10-389-566-1240			
; Sequence 1240, Application US/10389566			
; Publication No. US20040025202A1			
; GENERAL INFORMATION:			
; APPLICANT: Monsanto Technology, LLC			
; APPLICANT: Laurie, Cathy C			
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants			
; FILE REFERENCE: 38-77(52900)D			
; CURRENT APPLICATION NUMBER: US/10/389,566			
; CURRENT FILING DATE: 2003-03-31			
; PRIOR APPLICATION NUMBER: US 60/365,301			
; PRIOR FILING DATE: 2002-03-15			
; PRIOR APPLICATION NUMBER: US 60/391,786			
; PRIOR FILING DATE: 2002-06-25			
; PRIOR APPLICATION NUMBER: US 60/392,018			
; PRIOR FILING DATE: 2002-06-26			
; NUMBER OF SEQ ID NOS: 2459			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 1240			
; LENGTH: 282			
; TYPE: PRT			
; ORGANISM: Arabidopsis thaliana			
US-10-389-566-1240			
Query Match 50.9%; Score 921.5; DB 15; Length 282;			
Best Local Similarity 63.7%; Pred. No. 3e-67;			
Matches 174; Conservative 42; Mismatches 50; Indels 7; Gaps 3;			
Qy	70	RHTTDDFEIGPLGKGFNNVLAAREKSHFIVALKVLFKSOIEKEGVEHQLRREIEIQ	129
Db	12	KWTTSDFDIGKPLGKGFHVLAREKTSNHIIVALKVLFKSOIQSQVQLRREIEIQ	71
Qy	130	AHLHPNLRILNYFYDRRIILILEYAPRGELYKELQKCTFDEQRTATIMEELADLM	189
Db	72	SHLRHPNLRILYGYFYDQKRVLLILEYAPRGELYKELQKCYFSERRAATVVASLARALI	131
Qy	190	YCHGKGVHRIKIPENLLILGKELKIADFGWSVHAPSRLRKTMCCTGLDYLPPMIEGRM	249
Db	132	YCHGKGVHRIKIPENLLILGKELKIADFGWSVHTFN-RRRTMCGTGLDYLPPMIEGRM	190
Qy	250	HNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKDLKFPAS--VPTGAODLISKL	307
Db	191	HDASVDIWSLGVLCYFLLGVPPFEAREHSTYRRIIVQDLKFPKPIVSSAKDLISQM	250
Qy	308	LRHNPSEIRPLAQVSAHPWVRANSRRLPPSAL 340	
Db	251	LVKESTQRLALHLKLEHPWIVQNA----DPSGL 279	
RESULT 44			
US-10-389-566-382			
; Sequence 382, Application US/10389566			
; Publication No. US20040025202A1			
; GENERAL INFORMATION:			
; APPLICANT: Monsanto Technology, LLC			
; APPLICANT: Laurie, Cathy C			
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants			
; FILE REFERENCE: 38-77(52900)D			
; CURRENT APPLICATION NUMBER: US/10/389,566			
; CURRENT FILING DATE: 2003-03-31			
; PRIOR APPLICATION NUMBER: US 60/365,301			
; PRIOR FILING DATE: 2002-03-15			
; PRIOR APPLICATION NUMBER: US 60/391,786			
; PRIOR FILING DATE: 2002-06-25			
; PRIOR APPLICATION NUMBER: US 60/392,018			
; PRIOR FILING DATE: 2002-06-26			
; NUMBER OF SEQ ID NOS: 2459			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 382			
; LENGTH: 368			
; TYPE: PRT			
; ORGANISM: Zea mays			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)..(1)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (9)..(9)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (48)..(48)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (56)..(56)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (86)..(87)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (86)..(87)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (86)..(87)			
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid			
; FEATURE:			
; NAME/KEY			

US-10-389-566-382

Query Match 50.7%; Score 918; DB 15; Length 368;
Best Local Similarity 58.8%; Pred. No. 8e-67;
Matches 177; Conservative 47; Mismatches 59; Indels 18; Gaps 4;

QY 48 OPT--NAPGQKVNENSGTPDIL-----TRHTIDDPEIGRPLGKKGQNVY 92
DB 57 RPHASPSAPLHNGGHRVARQGGQKXSHANOEKRWLSDFVGKPLGRKGFHVV 116
QY 93 LAREKSHFTVALKVLFKSQIEKEGVEHQLRREIEIOAHLHHPNIRLNYFYDRRIYL 152
DB 117 LAREKSSSEVALKVLFKSQSQVHQLRREVEIQSHLRHPIRLNYGYFDQTRVYL 176
QY 153 ILEYAPRGELYKELQKSCFTDEORTATIMBELADALMYCHGKKVHHRDIKPNLLGLKG 212
DB 177 ILEYAAKGELYKELTRCKHPSERTATYVASLARALYILHGHVHHRDIKPNLLGVQG 236
QY 213 ELKIADPGSVHAPSRRRTKTCGTIDYLPPEMIEGRHNEKVDLWICIGVLCYELLVGNPP 272
DB 237 EIKIADFGSVHTFN--RRRTMCGTLDYLPPEMVEKAEDYHVDIWSGLVLCYEFYGVPP 295
QY 273 FESASHNETYRRIVKVDLKPAS--VPTGAQDLISKLRHNPSERLPLAQVSAHPWVRAN 330
DB 296 FEAKEHSEYRRIVKVDLKPPLKPFVSPAADLIQSMLVKSQAORLPLHKLHPWIVQN 355
QY 331 S 331
DB 356 A 356

RESULT 45

US-10-389-566-819
; Sequence 819, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 819
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: misc feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-389-566-819

Query Match 50.7%; Score 917.5; DB 15; Length 418;
Best Local Similarity 65.2%; Pred. No. 1e-66;
Matches 172; Conservative 41; Mismatches 48; Indels 3; Gaps 2;

QY 70 RHFTDDPEIGRPLGKKGQNVYLAREKSHFTVALKVLFKSQIEKEGVEHQLRREIEIQ 129
DB 148 KRWLSDFDVGKPLGKGFHVLAREKSNHIVALKVLFKSQSQVHQLRREVEIQ 207
QY 130 AHLHHPNIRLNYFYDRRIYILLEYAPRGELYKELQKSCFTDEORTATIMEELADALM 189
DB 208 SHLRHPIRLNYGYFDQTRVYLILLEYALKGELYKELQCKHPSERRSATYASLAHALI 267
QY 190 YCHGKKVHHRDIKPNLLGLKGELKIADFGWSVHAPSRRRTMCGTLDYLPPEMIEGRM 249

DB 268 YLHGKHVIHRDIKPNLLIGSQGELKIADFGWSVHTFN--RRRTMCGTLDYLPPEMVEKTE 326
QY 250 HNEKVDLWICIGVLCYELLVGNPPFFESASHNETYRRIVKVDLKPAS--VPTGAQDLISKL 307
DB 327 HDYHVDIWSGLICYEFYGVPPFEAKEHSEYRRIVKVDLKPFLKPFVSPAADLIQSOM 386
QY 308 LRHNPSERLPLAQVSAHPWVRANS 331
DB 387 LVKNSAHRPLPLHKLHPWIVQNA 410

RESULT 46

US-10-437-963-133574
; Sequence 133574, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133574
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(320)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35430C.1.pap

US-10-437-963-133574

Query Match 50.7%; Score 916.5; DB 16; Length 320;
Best Local Similarity 65.2%; Pred. No. 9e-67;
Matches 172; Conservative 41; Mismatches 48; Indels 3; Gaps 2;

QY 70 RHFTDDPEIGRPLGKKGQNVYLAREKSHFTVALKVLFKSQIEKEGVEHQLRREIEIQ 129
DB 50 KRWLSDFDVGKPLGKGFHVLAREKSNHIVALKVLFKSQSQVHQLRREVEIQ 109
QY 130 AHLHHPNIRLNYFYDRRIYILLEYAPRGELYKELQKSCFTDEORTATIMEELADALM 189
DB 110 SHLRHPIRLNYGYFDQTRVYLILLEYALKGELYKELQCKHPSERRSATYASLAHALI 169
QY 190 YCHGKKVHHRDIKPNLLGLKGELKIADFGWSVHAPSRRRTMCGTLDYLPPEMIEGRM 249
DB 170 YLHGKHVIHRDIKPNLLIGSQGELKIADFGWSVHTFN--RRRTMCGTLDYLPPEMVEKTE 228
QY 250 HNEKVDLWICIGVLCYELLVGNPPFFESASHNETYRRIVKVDLKPAS--VPTGAQDLISKL 307
DB 229 HDYHVDIWSGLICYEFYGVPPFEAKEHSEYRRIVKVDLKPFLKPFVSPAADLIQSOM 288
QY 308 LRHNPSERLPLAQVSAHPWVRANS 331
DB 289 LVKNSAHRPLPLHKLHPWIVQNA 312

RESULT 47

US-10-424-599-274736
; Sequence 274736, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274736
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(307)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90107C.1.pap
US-10-424-599-274736
```

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Query Match          50.2%; Score 909; DB 15; Length 307;
Best Local Similarity 62.9%; Pred. No. 3.5e-66;
Matches 173; Conservative 44; Mismatches 44; Indels 14; Gaps 4;

QY 70 RHFTDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVEHOLRREIEIQ 129
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 26 RWTLNDFDIGKPLGRGKGFHVYLAREKTSNHIVALKVLFKSOLOQSQVQHRLRREVEIQ 85
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 130 AHLHPNIIRLNLYFYDRRRIYLIILEYAPRGELYKELQKSCCTFDEORTATIMEEL---- 184
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 86 SHLRHPHILRLYGYFYDQKRVYLILEYAPKGLYKELQCKYFSPERRAATYVASLEHLR 145

QY 185 -ADALMYCHGKK-----VTHRDIKPENLILGLKGLKIADFGWSVHAPSRLRRTKTCGTILD 238
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 146 FARALTYCHGKKEVTHFVTHRDIKPENLLMGAEGELKIADFGWSVHTFN--RRRTMCGTILD 204

QY 239 YLPPEMIEGRMNEKVDLCIGVLCYELVGNPPFSASHNETYRRIVKVDLKFPAS--V 296
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 205 YLPPEMVESVEHSDASVDIWSGLVCEFLYGVPPFPAKEHSDTYRIIQVDLKFPPKPIV 264

QY 297 PTGAQDLISKLRLHPNPSERLPLAQVSAHPWVRANS 331
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 265 SSAAKDLISQMLVKDSSQRLPLHLKLEHPWIVQNA 299
```

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RESULT 48
US-10-389-566-550
; Sequence 550, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 550
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (130)..(130)
```

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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (135)..(135)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-550

Query Match          50.2%; Score 908; DB 15; Length 298;
Best Local Similarity 63.7%; Pred. No. 4.1e-66;
Matches 170; Conservative 45; Mismatches 46; Indels 6; Gaps 3;

QY 70 RHFTDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVEHOLRREIEIQ 129
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 25 RWTLNDFDIGKPLGRGKGFHVYLAREKTSNHIVALKVLFKSOLOQSQVQHRLRREVEIQ 84
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 130 AHLHPNIIRLNLYFYDRRRIYLIILEYAPRGELYKELQKSCTF--DEORTATIMEELAD 186
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 85 SHLRHPHILRLYGYFYDQKRVYLILEYAPKGLYKELQCKYFSPERRAXATYVASLAR 144

QY 187 ALMYCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIE 246
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 145 ALIYCHGKHVIHRDIKPENLLIGAQELKIADFGWSVHTFN--RRRTMCGTLDYLPPEMVE 203

QY 247 GRMNEKVDLCIGVLCYELVGNPPFSASHNETYRRIVKVDLKFPAS--VPTGAQDLI 304
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 204 SYEHSDASVDIWSGLVCEFLYGVPPFPAKEHSDTYRIIQVDLKFPPKPIVSSAAKDLI 263

QY 305 SKLLRHPNPSERLPLAQVSAHPWVRANS 331
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 264 SQMLVKDSSQRLPLHLKLEHPWIVQNA 290
```

```

RESULT 49
US-10-389-566-2420
; Sequence 2420, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2420
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-389-566-2420
```

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Query Match          50.1%; Score 906; DB 15; Length 432;
Best Local Similarity 65.2%; Pred. No. 9.3e-66;
Matches 172; Conservative 40; Mismatches 48; Indels 4; Gaps 3;

QY 70 RHFTDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVEHOLRREIEIQ 129
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 163 KRWLSDFDIGKPLGRGKGFHVYLAREKTSNHIVALKVLFKSOLOQSQVQHRLRREVEIQ 222
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 130 AHLHPNIIRLNLYFYDRRRIYLIILEYAPRGELYKELQKSCCTFDEORTATIMEELADLM 189
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 223 SHLRHPNIIRLYGYFYD--TRVYLIILEYALKGELYKELQCKYFSPERRSATYIASLAHALI 281

QY 190 YCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSRLRRTKTCGTLDYLPPEMIEGRM 249
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 282 YLHGKVIHRDIKPENLLIGSQELKIADFGWSVHTFN--RRRTMCGTLDYLPPEMVEKTE 340
```

Qy	250	HNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKEPAS--VPTGAODLISKL	307
Db	341	HDYHVDIWSLGLICYEFLYGVPPFEAKHSETYRRIVKVDLKEPFLKPFVSPAAKDLISQM	400
Qy	308	LRHNPSERLPLAQVSAHPWVRANS	331
Db	401	LKNSAHLPLHKLEHPWIVQNA	424

Search completed: June 20, 2005, 20:06:50
Job time : 72.8132 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:57:12 ; Search time 118.351 Seconds
(without alignments)
1488.417 Million cell updates/sec

Title: US-10-734-126-3
Perfect score: 1809
Sequence: 1 MAQKNSYWPVGYROTAPSG.....PWVRRNSRVLPSPALQSWA 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 33

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%
Maximum Match 100%
Listing first 65000 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	344	1 AURB HUMAN	Q96gd4 homo sapien
2	1670	92.3	344	2 Q7YRC6	Q7YRC6 bos taurus
3	1664	92.0	344	2 Q7YRC7	Q7YRC7 sus scrofa
4	1525.5	84.3	345	1 AURB MOUSE	Q70126 mus musculus
5	1520.5	84.1	343	1 AURB RAT	O55099 rattus norv
6	1519.5	84.0	345	2 Q8C6C1	Q8C6C1 mus musculus
7	1239	68.5	361	2 Q8DE08	Q6d608 xenopus lae
8	1239	68.5	371	2 Q7ZYT9	Q7zyt9 xenopus lae
9	1238	68.4	361	2 Q9DF70	Q9df70 xenopus lae
10	1237	68.4	361	2 Q8JG74	Q8jg74 xenopus lae
11	1234.5	68.2	368	2 Q6GPL3	Q6gpl3 xenopus lae
12	1230	68.0	309	1 AURC HUMAN	Q9ubp9 homo sapien
13	1222	67.6	289	2 Q6AZF8	Q6azy8 homo sapien
14	1222	67.6	290	2 Q6DLZ0	Q6dlz0 homo sapien
15	1156	63.9	320	2 Q6NW76	Q6nw76 brachydanio
16	1154	63.8	282	1 AURC MOUSE	Q88445 mus musculus
17	1147	63.4	276	2 Q6P209	Q6p209 mus musculus
18	1111.5	61.4	346	2 Q8JGS8	Q8jgs8 brachydanio
19	1084	59.9	395	1 STK6 MOUSE	P97477 mus musculus
20	1084	59.9	395	2 Q7TNK2	Q7tnk2 mus musculus
21	1080	59.7	386	2 Q8C3H8	Q8c3h8 mus musculus
22	1073	59.3	395	2 Q8BP87	Q8bp87 mus musculus
23	1071	59.2	397	1 STK6 RAT	P59241 rattus norv
24	1062	58.7	408	1 STK6_XENLA	Q91819 xenopus lae
25	1060	58.6	408	2 Q6BUK0	Q6bjk0 xenopus lae
26	1057.5	58.5	403	1 STK6 HUMAN	O14965 homo sapien
27	1050.5	58.1	407	1 STK6_XENLA	Q91820 xenopus lae
28	1041.5	57.6	405	2 Q6DBZ4	Q6dbz4 brachydanio
29	940	52.0	294	2 Q9M077	Q9m077 arabidopsis
30	937	51.8	294	2 Q8L5X4	Q8l5x4 arabidopsis
31	921.5	50.9	282	2 Q82309	Q82309 arabidopsis

32 921.5 50.9 288 2 Q683C9 Q683c9 arabidopsis
33 906 50.1 432 2 Q9LG71 Q9lg71 oryza sativ

ALIGNMENTS

```
RESULT 1
AURB_HUMAN
ID AURB_HUMAN STANDARD; PRT; 344 AA.
AC Q96GD4; O14630; O60446; Q95083; Q96DVS; Q9UQ46;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase
DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).
GN Name-AURKB; Synonyms-AIK2, AIM1, ARK2, STK12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2".
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99025855; PubMed=9809983;
RA Tataka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
RT aurora- and Ipl1-like midbody-associated protein mitotic kinase in
RT human cancer cells".
RL Cancer Res. 58:4811-4816(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Spleen;
RX MEDLINE=99077743; PubMed=9858806;
RA Kimura M., Matsuda Y., Yoshioka T., Sumi N., Okano Y.;
RT "Identification and characterization of STK12/Aik2: a human gene
RT related to aurora of Drosophila and yeast IPL1".
RL Cytogenet. Cell Genet. 92:147-152(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21364697; PubMed=11471245;
RA Prigent C., Gill R., Tower M., Sanseau P.;
RT "In silico cloning of a new protein kinase, Aik2, related to
RT Drosophila aurora using the new tool: EST Blast.".
RN In Sillico Biol. 1:123-128(1999).
RP SEQUENCE FROM N.A.
RX Zhang Q., Yu L., Bi A.;
RT "Cloning of a novel human gene homologous to mouse STK-1.";
RN Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=lung, Lymph, and Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Brakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RX MEDLINE=21306577; PubMed=11413462; DOI=10.1038/35048096;
RY Nigg E.A.,
RT "Mitotic kinases as regulators of cell division and its checkpoints.";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC -!- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body.
CC -!- TISSUE SPECIFICITY: High level expression seen in the thymus. It
CC is also expressed in the spleen, lung, testis, colon, placenta and
CC fetal liver. Expressed during S and G2/M phase and expression is
CC up-regulated in cancer cells during M phase.
CC -!- DISEASE: Disruptive regulation of expression is a possible
CC mechanism of the perturbation of chromosomal integrity in cancer
CC cells through its dominant-negative effect on cytokinesis.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF008552; AAC12709.1; -
CC EMBL; AB011450; BAA32136.1; -
CC EMBL; AB011446; BAA82709.1; -
CC EMBL; AF004022; AAB65786.1; -
CC EMBL; AF015254; AAC98891.1; -
CC EMBL; BC000442; AAH00442.2; ALT_INIT.
CC EMBL; BC009751; AAH09751.1; -
CC EMBL; BC013300; AAH13300.2; ALT_INIT.
CC HSSP; P31751; IGZK.
CC Genew; HGNC:11390; AURKB.
CC H-InvDB; HIX0019005; -
CC MIM; 604970; -
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Cell cycle; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 77 327 protein kinase.
FT BIND 83 91 ATP (By similarity).
FT BINDING 106 106 ATP (By similarity).
FT ACT_SITE 200 200 Proton acceptor (By similarity).
FT CONFLICT 14 15 RQ -> DK (in Ref. 5).
FT CONFLICT 70 70 R -> RR (in Ref. 6; AAH13300).
FT CONFLICT 161 161 E -> M (in Ref. 4 and 5).
FT CONFLICT 167 169 QKS -> HKT (in Ref. 4).
FT

FT CONFLICT 179 179 T -> TVRR (in Ref. 4).
FT CONFLICT 180 180 I -> VRV (in Ref. 5).
FT CONFLICT 226 226 P -> T (in Ref. 3).
FT CONFLICT 249 250 MH -> ID (in Ref. 3).
FT CONFLICT 271 271 Missing (in Ref. 3).
FT CONFLICT 298 298 T -> M (in Ref. 6; AAH09751/AAH13300).
SQ SEQUENCE 344 AA; 39280 MW; 8325E3EF5A1FB170 CRC64;
Query Match 100.0%; Score 1809; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.2e-123;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKNSYWPYGRQTAPSGSLTLPQVLRKEPVTPTPSALVLMRSNVQTAAPGQKVMEN 60
DB 1 MAQKNSYWPYGRQTAPSGSLTLPQVLRKEPVTPTPSALVLMRSNVQTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFQNVYLAREKSHFIVALKVLFKSIKEGVEH 120
DB 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFQNVYLAREKSHFIVALKVLFKSIKEGVEH 120
QY 121 QLRRETIQAHLLHHPNLLNLYFYDRRIYLLILEVAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETIQAHLLHHPNLLNLYFYDRRIYLLILEVAPRGELYKELQKCTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVHRDIKPNLLGLKGLKELKIADFGWSVHAPSLRRKTCGTL 240
DB 181 MEELADALMYCHGKVKVHRDIKPNLLGLKGLKELKIADFGWSVHAPSLRRKTCGTL 240
QY 241 PEMIEGRMHNEKVDLWCIGVLCYELLVGNPFPSASHNETYRRIVKVDLKPASVPTGA 300
DB 241 PEMIEGRMHNEKVDLWCIGVLCYELLVGNPFPSASHNETYRRIVKVDLKPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRNSRRVLPSPSALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRNSRRVLPSPSALQSV 344
RESULT 2
QYRC6 PRELIMINARY; PRT; 344 AA.
AC QYRC6;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Serine/threonine kinase 12.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Li W., Yu L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY336975; AAQ16151.1; -
DR HSSP; O14965; 1OL6
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 344 AA; 39441 MW; 4DD7158CF2F5D047 CRC64;
Query Match 92.3%; Score 1670; DB 2; Length 344;
Best Local Similarity 93.0%; Pred. No. 2.8e-113;
Matches 319; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
QY 1 MAQKENSYPYGRQTAPSGLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKWMEN 60
DB 1 MAQKENTYPYGRQTAPSGLTLPQVLRKEA VTPSALVLMRSNTQPTAAPGQKVVEN 60
QY 61 SSGTPTDILTRHFTDIDDEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVEH 120
DB 61 SSGTPTNFSTRFTDIDDEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVEH 120
QY 121 QLRREIEIOAHLHPNLRILYNYFYDRRRYILILEYAPRGELYKELQKSTFDEQRTATI 180
DB 121 QLRREIEIOAHLHPNLRILYNYFYDRRRYILILEYAPRXELYKELQKSTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLILGLKGBELKIADFGWSVHAPSRLRKTMCCTLDYL 240
DB 181 MEELADALYIYCHGKVKVTHRDIKPENLILGLKGBELKIADFGWSVHAPSRLRKTMCCTLDYL 240
QY 241 PPMIEGRMNEKVDLWCIGVLCVELLVGNPPPSASHNETYRRIKVKVDLKEPASVPTGA 300
DB 241 PPMIEGRTHNEKVDLWCIGVLCVELLVGNPPPSASHNETYRRIKVKVDLKEFPSPVPAGA 300
QY 301 QDLISKLLRHPNRPSEPLAQVSAHPWVRNRRVLPSPALQSV 343
DB 301 QDLISKLLKHPNRPSEPLAQVSAHPWVRNRRVLPSPAPQSV 343
RESULT 3
QYRC7 PRELIMINARY; PRT; 344 AA.
AC QYRC7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine kinase 12.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Li W., Yu L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY336974; AAQ16150.1; -;
DR HSSP; O14965; 1OL6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR02052; N6_Mtase.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_A5.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 344 AA; 39275 MW; 5CEC29C50C307F12 CRC64;
Query Match 92.0%; Score 1664; DB 2; Length 344;
Best Local Similarity 92.7%; Pred. No. 7.6e-113;
Matches 318; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAQKENSYPYGRQTAPSGLTLPQVLRKEPVTSPALVLMRSNVQPTAAPGQKWMEN 60
DB 1 MAQKENTYPYGRQTAPSGLTLPQVLRKEA VTPSALVLMRSNTQPTAAPGQKVVEN 60
QY 61 SSGTPTDILTRHFTDIDDEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVEH 120
DB 61 SSGTPTNFSTRFTDIDDEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVEH 120
QY 121 QLRREIEIOAHLHPNLRILYNYFYDRRRYILILEYAPRGELYKELQKSTFDEQRTATI 180
DB 121 QLRREIEIOAHLHPNLRILYNYFYDRRRYILILEYAPRXELYKELQKSTFDEQRTATI 180
QY 181 MEELADALMYCHGKVKVTHRDIKPENLILGLKGBELKIADFGWSVHAPSRLRKTMCCTLDYL 240
DB 181 MEELADALYIYCHGKVKVTHRDIKPENLILGLKGBELKIADFGWSVHAPSRLRKTMCCTLDYL 240
QY 241 PPMIEGRMNEKVDLWCIGVLCVELLVGNPPPSASHNETYRRIKVKVDLKEFPASVPTGA 300
DB 241 PPMIEGRTHNEKVDLWCIGVLCVELLVGNPPPSASHNETYRRIKVKVDLKEFPSPVPAGA 300
QY 301 QDLISKLLRHPNRPSEPLAQVSAHPWVRNRRVLPSPALQSV 343
DB 301 QDLISKLLKHPNRPSEPLAQVSAHPWVRNRRVLPSPAPQSV 343
RESULT 4
AURB MOUSE STANDARD; PRT; 345 AA.
AC Q70136; Q61882;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase 12 (EC 2.7.1.37) (Aurora-related kinase 2) (Serine/threonine-protein kinase 5) (STK-1) (Aurora-B).
DE Name=Aurkb; Synonyms=Ark2, Stk1, Stk12, Stk5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Testis;
RX MEDLINE=96194801; PubMed=8647446; DOI=10.1016/0378-1119(95)00809-8;
RA Niwa H., Abe K., Kunitada T., Yamamura K.;
RT "Cell-cycle-dependent expression of the STK-1 gene encoding a novel murine putative protein kinase."
RL Gene 169:197-201(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M., Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal assignment of mammalian aurora homologues, aurora-related kinase (ARK) 1 and 2."
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Spapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

[illegible]


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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22209728; PubMed=12221116;
RA Bolton M.A., Lan W., Powers S.E., McClelland M.L., Kuang J.,
RA Stukenberg P.T., exists in a complex with survivin and INCENP and its
RT kinase activity is stimulated by survivin binding and
RT phosphorylation."
RL Mol. Biol. Cell 13:3064-3077(2002).
CC 1-1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY115554; AM76715.1; -.
DR HSSP; O14965; 1OL6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 361 AA; 41777 MW; 1FB77E41E1D07E8 CRC64;

Query Match 68.4%; Score 1237; DB 2; Length 361;
Best Local Similarity 68.9%; Pred. No. 8.6e-82;
Matches 244; Conservative 39; Mismatches 53; Indels 18; Gaps 6;

QY 1 MAQKENSYPWPY-GROTAPSGLTLPQVLRLKEP-----VTPSALVLMGR---SNVOPTA 51
Db 1 MEYKENLNPSYTSKFTTSS-ATAQVRLRLKEPYVSTFTTSDNLLAQRTQLSRTPSA 59
QY 52 A---PQO-----KVMENSSGTPDILTRHTTIDDFEIGRLPGKFGNVLAREKKSHTIV 103
Db 60 SSSVPGRVAVSTEMPSONTALAEMPXKFTTIDDFIGRLPGKFGNVLAREKQNKFM 119
QY 104 ALKVLFSQLEKEGVHQLRREIEIOAHLHPHNLRYNRYFYDRRIYLLILEVAPRGELY 163
Db 120 ALKVLFSQLEKEGVHQLRREIEIOAHLHPHNLRYNRYFYDRRIYLLILEVAPRGELY 179
QY 164 KELOKCTFDQRTATIMEELADALMYCHGKVIHRDIPENLLGLKGLKTADFGWSV 223
Db 180 KELOKGRFDEQSATFMELADALHYCHERKVIHRDIPENLLMGKGLKTADFGWSV 239
QY 224 HAPSLRRKTCGLDYLPPEMIEGRMHNEKVDLWLCVGLCYELLVGNPPFESASHNETYR 283
Db 240 HAPSLRRRTMCGLDYLPPEMIEGKTHDEKVDLWLCAGVLCYELVGMPPFSPSHETHR 299
QY 284 RIVKVDLKPPASVPTQAQDLISKLRHNSERLPLAQVSAHPVWVANSRRVLPP 337
Db 300 RIVNVDLKFPFLSDGSKDLISKLRHYHPQRLPLKGVMEHPVWVANSRRVLPP 353

RESULT 11
Q6GPL3 PRELIMINARY; PRT; 368 AA.
AC Q6GPL3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC83575 protein.
GN Name=MGC83575;
OS Xenopus laevis (African clawed frog).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Oocytes;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Oocytes;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Oocytes;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC 1-1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 42015 MW; D1E79FB995701214 CRC64;
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Query Match 68.2%; Score 1234.5; DB 2; Length 368;
Best Local Similarity 66.4%; Pred. No. 1.3e-81;
Matches 239; Conservative 40; Mismatches 58; Indels 23; Gaps 3;

QY 1 MAQKENSYPWPYGRGTAPS-----GLSTLPQVLRLKEP-----VTPSALVLMGRSNVQP 49
Db 1 MSYKENLIESSCSSSSSSSSSKFATSSATAAQVRLKQPVVSTFTTSDNLLAQRAQLAP 60
QY 50 TAAP-----GQKVMENSSGTPDILTRHTTIDDFEIGRLPGKFGNVLAREK 97
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Db 61 RVTPAASSVPGRVAGTVDVASHNTALAEAPKPKFFIDDDIGRPLGKGFNGVYLAREK 120
Qy 98 KSHFIVALKVLFKSQIEKEGVEHQLRREIEIQHLHPNLRNLYNYFYDRRRYLLILEVA 157
Db 121 QNKFINALKVLFKSQIEKEGVEHQLRREIEIQHLHPNLRNLYNYFYDRKRILYLMLEFA 180
Qy 158 PRGELYKELKSTCFDQRTATTMEELADALMYCHGKVKVHRDIKBPENLLGLKGLKIA 217
Db 181 PRGELYKELQKGRFQDSATFMEELADALQYCHERKVIHRDKPENLLMYGKGLKIA 240
Qy 218 DFGWSVHAPSRLRKTWCGTLDYLPPEMIEGRMEKVDLWCIGVLCYELLVGNPPFESAS 277
Db 241 DFGWSVHAPSRLRKTWCGTLDYLPPEMIEGKTHDEKVDLWCAGVLCYELLVGNPPFDS 300
Qy 278 HNTYTRIRVKVDLKFPAASVPTGQADLSKILRLHNPSEPLAQVSAHPWVRANSRRLVPP 337
Db 301 HSETHRRIVNVDLKFPPFLSEGSKDLKILRLVHPAQLPKGVMEHPWVKANSRRLVPP 360

RESULT 12
AURC HUMAN
ID AURC HUMAN STANDARD; PRT; 309 AA.
AC Q9UQ89; O60681; O75442; Q9UPK5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Serine/threonine-protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
protein 2) (Aurora/Ipl1-related kinase 3) (Aurora-C).
GN Name=AURKC; Synonyms=AIE2, AIK3, STK13;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.-C., Chen S.-H., Hsu Y.-P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
characterization of two novel testis-specific protein kinases (AIE1,
AIE2) related to yeast and fly chromosome segregation regulators."
RL DNA Cell Biol. 17:823-833 (1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=99017981; PubMed=9799611; DOI=10.1006/geno.1998.5522;
RA Bernard M., Sansau P., Henry C., Couturier A., Prigent C.;
RT "Cloning of STK13, a third human protein kinase related to Drosophila
aurora and budding yeast Ipl1 that maps on chromosome 19q13.3-tex."
RL Genomics 53:406-409 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=99167501; PubMed=10066797; DOI=10.1074/jbc.274.11.7334;
RA Kimura M., Matsuda Y., Yoshioaka T., Okano Y.;
RT "Cell cycle-dependent expression and centrosome localization of a
third human Aurora/Ipl1-related protein kinase, AIK3."
RL J. Biol. Chem. 274:7334-7340 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
Caenepeel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M.,
Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,
Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

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RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
Slezak T., Solovye V., Thayer N., Tice K., Tsai M., Uataszewska A.,
Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Zebach I.,
Furey T.S., Dedong P., Dickson M., Gordon D., Eichler E.E.,
Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19."
RL Nature 428:529-535 (2004).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to centrosome from anaphase to
cytokinesis.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UQ89-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UQ89-2; Sequence=VSP_004872;
CC -!- TISSUE SPECIFICITY: Expression is limited to testis. Elevated
expression levels were seen only in a subset of cancer cells such
as HepG2, HuH7 and HeLa cells. Expression is maximum at M phase.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF054621; AAC25955.1; -;
CC EMBL; AF059681; AAC77369.1; -;
CC EMBL; AB017332; BAA76292.1; -;
CC DR EMBL; AC005261; -; NOT_ANNOTATED_CDS.
CC DR HSSP; P49137; 1KWP.
CC DR Genew; HGNC:11391; AURKC.
CC DR MIM; 603495; -;
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Kinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC KW Alternative splicing; ATP-binding; Cell cycle;
Serine/threonine-protein kinase; Transferase.
FT DOMAIN 43 293
FT NP_BIND 49 57
FT BINDING 72 72
FT ACT_SITE 166 166
FT VARSPPLIC 1 34
FT CONFLICT 109 109
FT CONFLICT 150 150
FT CONFLICT 193 195
FT SEQUENCE 309 AA; 35591 MW; 41B7DFCA91704201 CRC64;
SQ
Query Match 68.0%; Score 1230; DB 1; Length 309;
+ Best Local Similarity 76.7%; Pred. No. 2.3e-81;
Matches 237; Conservative 27; Mismatches 35; Indels 10; Gaps 3;
Qy 35 TPSALVLMRSNVQPT----AAPGKVMNSGSTPDILTRHFTIDDFEIGRPLGKGFNG 90
Db 3 SPRAVVLQJKA--QPAGEELATANTAQQPSPA-----MRLTVDDDFEIGRPLGKGFNG 56
Qy 91 VYLAREKKSHTFVAVKLVFKSQIEKEGVEHQLRREIEIQHLHPNLRNLYNYFYDRRRI 150

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Db 57 VYLARKESHFIVALKVLFKSIQIEGLEHQRREIEIQAHLOHPNILRLNYFHDARRV 116
QY 151 YLILEYAPRGELYKELQKSTFDEORTATIMELADALMYCHGKKVIHRDIPENLLGL 210
Db 117 YLILEYAPRGELYKELQKSEKDEORTATIMELADALTYCHDKKVIHRDIPENLLGF 176
QY 211 KGELKIADFGWSVHAPSLRRKTCGTLDPPEMIEGRMHNEKVDLWCIGVLCEYLLVGN 270
Db 177 RGEVKIADFGWSVHTPSLRKTCGTLDPPEMIEGRTYDEKVDLWCIGVLCEYLLVGY 236
QY 271 PPFESASHNETRYRIVKVLKPPASVPTCAQDLISKLRLHNPSEIRPLAQSVAHPWVRAN 330
Db 237 PPFESASHSETRYRILKVDVRFPLSPGLGARDLISRLRYQPLERPLAQILKHPWVAH 296
QY 331 SRRVLPPSA 339
Db 297 SRRVLPPCA 305
RESULT 13
Q6AZV8 PRELIMINARY; PRT; 289 AA.
AC Q6AZV8 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC075064; AAH75064.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR QY

ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 289 AA; 33542 MW; 70303465BB285F7D CRC64;
Query Match 67.6%; Score 1222; DB 2; Length 289;
Best Local Similarity 84.4%; Pred.No. 8.1e-81;
Matches 228; Conservative 21; Mismatches 21; Indels 0; Gaps 0;
QY 70 RHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIQIEGLEHQRREIEIQ 129
Db 16 RRLTWDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSIQIEGLEHQRREIEIQ 75
QY 130 AHLHPNILLRLNYFYDRRIYLIILEYAPRGELYKELQKSTFDEORTATIMEELADALM 189
Db 76 AHLQHPNILLRLNYFHDARRVYLILEYAPRGELYKELQKSEKLEDEORTATIMEELADALT 135
QY 190 YCHGKKVIHRDIPENLLGLKELKIADFGWSVHAPSLRRKTCGTLDPPEMIEGRM 249
Db 136 YCHDKKVIHRDIPENLLGLFGEVKIADFGWSVHTPSLRKTCGTLDPPEMIEGRM 195
QY 250 HNEKVDLWCIGVLCEYLLVGNPPESASHNETRYRIVKVDLKPASVPTCAQDLISKLRL 309
Db 196 YDEKVDLWCIGVLCEYLLVGNPPESASHSETRYRILKVDVRFPLSPGLGARDLISRLR 255
QY 310 HNPSEIRPLAQSVAHPWVRANSRRVLPPSA 339
Db 256 YQPLERLPLAQILKHPWVAHSSRRVLPPCA 285
RESULT 14
Q6DLZ0 PRELIMINARY; PRT; 290 AA.
AC Q6DLZ0 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aurora/Ipl1-related kinase 3 transcript variant 1.
GN Name=AURKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yan X., Cao L., Yu L.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY661554; AAT64422.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 290 AA; 33672 MW; D07PD6988E208140 CRC64;

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Query Match      67.6%; Score 1222; DB 2; Length 290;
Best Local Similarity 84.4%; Pred. No. 8.1e-81;
Matches 228; Conservative 21; Mismatches 21; Indels 0; Gaps 0;

QY 70 RHFTDIDFEIGRLPGKGGKGNVYLAREKSHFIVALKVLPKSOIEKEGVHQLRREIEIQ 129
   |.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 17 RRLTVDDFEIGRLPGKGGKGNVYLAREKSHFIVALKVLPKSOIEKEGVHQLRREIEIQ 76

QY 130 AHLHPNLRILYNYFYDRRIYILLEYAPRGELYKELQKSCTFDQRTATIMEELADALM 189
   |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 77 AHLQHPNLRILYNYFYDRRIYILLEYAPRGELYKELQKSCTFDQRTATIMEELADALT 136

QY 190 YCHGKKVHHDIDKPNLILGLKGLKTIADFGWSVHAPSLRRKTCGTLDYLPPEMTEGRM 249
   |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 137 YCHDKKVIHHDIDKPNLILGLKGLKTIADFGWSVHAPSLRRKTCGTLDYLPPEMTEGR 196

QY 250 HNEKVDLWCIGVLCYELLVGNPPSPESASHNETYRRIYKVDLPKPPASVPTGAQDLISKLR 309
   |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 197 YDEKVDLWCIGVLCYELLVGNPPSPESASHNETYRRIYKVDLPKPPASVPTGAQDLISKLR 256

QY 310 HNPSERLPLAQVSAHPMVRANSRRVLPSPA 339
   :.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 257 YQPLERPLAQILKHPWQAHRRVLPPCA 286

RESULT 15
Q6NW76 PRELIMINARY; PRT; 320 AA.
AC Q6NW76;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Serine/threonine kinase A.
GN Name:stka;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young J.W., Green E.D., Dickson M.C.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Shalaka U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC067695; AAH67695.1; -.
DR HSSP; Q63450; IA06.
DR ZFIN; ZDB-GENE-020419-40; stka.

```

GO: 0005524; F-ATP binding; IEA.
GO: 0004674; F-protein serine/threonine kinase activity; IEA.
GO: 0004713; F-protein-tyrosine kinase activity; IEA.
GO: 0016740; F-transferase activity; IEA.
GO: 0006468; P-protein amino acid phosphorylation; IEA.
InterPro: IPR011009; Kinase like.
InterPro: IPR02052; N6_Mcase.
InterPro: IPR00719; Prot_kinase.
InterPro: IPR02290; Ser_thr_kinase.
InterPro: IPR008271; Ser_thr_kinase.
InterPro: IPR001245; Tyr_kinase.
Pfam: PF00069; Pkinase; I.
ProDom: PD000001; Prot_kinase; 1.
SMART: SM00220; S_TKC; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SSQUENCE 320 AA; 36946 MW; D1D9EC08556D1CF1 CRC64;

Query Match 63.9%; Score 1156; DB 2; Length 320;
Best Local Similarity 66.9%; Pred. No. 5.7e-76;
Matches 228; Conservative 33; Mismatches 48; Indels 32; Gaps 4;

QY 1 MAQKNSYMPWYGRQTAPSGSLTPQRLKPEVTPSALVMSRSNVQP----TAAPGQK 56
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 1 MQNKENREP-----RVQO-----TPSAGVGLRVEKMPDTHAVSGPGRV 39

QY 57 VMENSGTDPDLTRHTTIDDPEIGRLPGKGGKGNVYLAREKSHFIVALKVLPKSOIEKE 116
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 40 PVKSNS-----KVLSDIDDFDGRPLGKGGKGNVYLAREKSHFIVALKVLPKSOIEKE 92

QY 117 GVEHQLRREIEIOAHLHPNLRILYNYFYDRRIYILLEYAPRGELYKELQKSCTFDQRT 176
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 93 GVEHQLRREIEIOAHLHPNLRILYNYFYDRRIYILLEYAPRGELYKELQKSCTFDQRT 152

QY 177 TATIMEELADALMCHYGKVIHHDIDKPNLILGLKGLKTIADFGWSVHAPSLRRKTCGT 236
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 153 TATIMEELADALMCHYGKVIHHDIDKPNLILGLKGLKTIADFGWSVHAPSLRRKTCGT 212

QY 237 LDVLPPEMTEGRMNEKVDLWCIGVLCYELLVGNPPSPESASHNETYRRIYKVDLPKPPASV 296
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 213 LDVLPPEMTEGRMNEKVDLWCIGVLCYELLVGNPPSPESASHNETYRRIYKVDLPKPPASV 272

QY 297 PTGAQDLISKLRHNPSERLPLAQVSAHPMVRANSRRVLPSP 337
 |||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.
Db 273 SEGARDLISKLRHNPSERLPLAQVSAHPMVRANSRRVLPSP 313

RESULT 16
AURC_MOUSE STANDARD; PRT; 282 AA.
AC O88445; Q9JULC2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
protein 1) (Aurora-C).
GN Name=Aurkc; Synonyms=AIE1, Stk13;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1,
RT AIE2) related to yeast and fly chromosome segregation regulators.";

Db 1 MEPSTST----RKHTINDFEIGRPLGRGKGRVYLARLKENHFIVALKVLFKSEIEKEG 56

Qy 118 VEHLQRRREIIOAHLHPNLRILNRYFYDRRRYLLILEYAPRGELYKELQKSCFTDEORT 177

Db 57 LEHLQRRREIIOAHLQHRNLRILNRYFYDDTRIVFLILEYAPRGEMYKELQRYG 172

Qy 178 ATMEELADALMYCHGKVKVTHRDIKPENLLGLKGLKGIADFGWSVHAPSRLRKTWCGLT 237

Db 117 ATIIQELSDALTVCHEKVKVTHRDIKPENLLGLNGEVIKISDFGWSVHTPSRLRKTWCGLT 176

Qy 238 DYLPPMEMIEGRMEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIIVKDLKFPASVP 297

Db 177 DYLPPEMIAQKPYNEWVDLWCIGVLCYELLVGNPPFESSSTSSYRRIIROVDKFPSSVP 236

Qy 298 TGAQDLISKLRNPSERPLAQVSAHPWVRANSRRVLP 336

Db 237 AGAQLISKLRYPHPSERLSLAQVLRKHPWVRHSRRVLP 275

RESULT 18

Q8UGS8 PRELIMINARY; PRT; 346 AA.

AC Q8UGS8

DT 01-OCT-2002 (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Aurora-like serine/threonine kinase (Fragment).

GN Name=stka;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=22035902; PubMed=12006978; DOI=10.1038/ng896;

RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,

RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,

RA Hopkins N.;

RT "Insertional mutagenesis in zebrafish rapidly identifies genes

RT essential for early vertebrate development."

RL Nat. Genet. 31:135-140(2002).

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AY099518; AB28206.1; -.

DR HSP; O14965; 10L6.

DR ZFIN; ZDB-GENE-020419-40; stka.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR002052; N6_Mtase.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_Thr_kinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

FT NON TER 1 1

SQ SEQUENCE 346 AA; 39977 MW; C8A2CEC221C7C2D9 CRC64;

Query Match 61.4%; Score 1111.5; DB 2; Length 346;

Best Local Similarity 73.2%; Pred. No. 1.1e-72;

Matches 210; Conservative 31; Mismatches 39; Indels 7; Gaps 1;

Qy 51 AAPGQKWMNSSTPDLTHFTFDPEGRPLGKGFNGVYLAREKKSHFIVALKVLFK 110

Db 60 SGGVRPVKSN-----KVLSDIDFDIGRPLGKGFNGVYLAREKKVIALKVLFK 112

RESULT 19

STRK6_MOUSE STANDARD; PRT; 395 AA.

AC P97477; O35624; Q91YU4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Aurora-family kinase

DE 1) (Aurora/IPLI-related kinase 1) (Ipli- and aurora-related kinase 1)

DE (Aurora-A) (Serine/threonine kinase Aykl).

GN Name=Stk6; Synonyms=Ark1, Aykl, Iak1;

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=BALB/c; TISSUE=Testis;

RX MEDLINE=97392693; PubMed=9245792; DOI=10.1083/jcb.138.3.643;

RA Gopalan G., Chan C.S.M., Donovan P.J.;

RT "A novel mammalian, mitotic spindle-associated kinase is related to

RT yeast and fly chromosome segregation regulators."

RL J. Cell Biol. 138:643-656(1997).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Testis;

RX MEDLINE=97349097; PubMed=9205101; DOI=10.1038/sj.onc.1201144;

RA Yanai A., Arama E., Kilfin G., Motro B.;

RT "aykl, a novel mammalian gene related to Drosophila aurora centrosome

RT separation kinase, is specifically expressed during meiosis."

RL Oncogene 14:2943-2950(1997).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=BALB/c;

RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;

RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,

RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;

RT "cDNA cloning, expression, subcellular localization, and chromosomal

RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)

RT 1 and 2."

RL Biochem. Biophys. Res. Commun. 244:285-292(1998).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RX MEDLINE=211306577; PubMed=11413462; DOI=10.1038/35048096;
RA Nigg E.A.;
RT "Mitotic kinases as regulators of cell division and its checkpoints.";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
and/or telophase, in relation to the function of the
centrosome/spindle pole region during chromosome segregation.
CC Maybe involved in microtubule formation and/or stabilization.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
and at each spindle pole in mitosis (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P97477-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P97477-2; Sequence=VSP_004871;
CC Note=May be less abundant or less stable;
CC -!- TISSUE SPECIFICITY: Highly expressed in testis, in about one third
of the seminiferous tubules. Expression is restricted to specific
spermatocytes nearing completion of prophase, with levels falling
off on transition to elongated spermatids. Highly expressed in the
ovary, expression in the oocyte starts around the transition to
large growing follicle. Abundant expression is seen in the
proliferating granulosa and thecal cells of the growing follicle,
and in the young corpus luteum. Very weakly expressed in spleen
and intestine.
CC -!- DEVELOPMENTAL STAGE: At 7.5-9.5 dpc expressed evenly all over the
embryo. At later stages, expression is mainly restricted to
proliferating zones. The highest levels of expression at mid-
embryonic development (13.5 dpc) were observed in the liver, lung,
kidney and back (trapezius) muscle and all regions in active
proliferation.
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U80932; AAB62982.1; -;
CC EMBL; AF007817; AAB63205.1; -;
CC EMBL; U69106; AAC12682.1; -;
CC EMBL; BC005425; AAB05425.1; -;
CC EMBL; BC014711; AAB14711.1; -;
CC EMBL; BC014711; AAB14711.1; -;
CC HSSP; P31751; IGZK.
CC MGD; MGI:894678; Stk6.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr pkin_AS.
CC InterPro; IPR002290; Ser Thr pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; Cell cycle; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 124 374 Protein kinase.
FT NP_BIND 130 138 ATP (By similarity).
FT BINDING 153 153 ATP (By similarity).
FT ACT_SITE 247 247 Proton acceptor (By similarity).
FT VARSPPLIC 1 1 M -> MAVEGEPCCCKRIGKAVRRGDM (in isoform
2).
FT /FTId=VSP_004871.
FT CONFLICT 234 234 A -> T (in Ref. 1).
SQ SEQUENCE 395 AA; 44772 MW; 2686B65105A1A812 CRC64;

Query Match 59.9%; Score 1084; DB 1; Length 395;
Best Local Similarity 62.7%; Pred. No. 1.3e-70;
Matches 210; Conservative 43; Mismatches 78; Indels 4; Gaps 2;

QY 6 NSYPMPYQGTAPSGSLTLPQRLKRPVTPSALVLMRSNVQPTAAPGQKVNENS--G 63
DB 51 NSQRPVSQAQKLGAGQKPAKQKLPAAASVPRPVSRLLNNPQKNEQPAASGNDSEKEQASLQK 110
QY 64 TDLILTRHTIIDDFEIGRLPGKKGNYLAREKKSHTFVALKVLKFSOIEKEGVHQLR 123
DB 111 TETDKRGWTFEDFDIGRLPGKKGNYLAREKKSHTFVALKVLKFSOIEKEGVHQLR 170
QY 124 REIEIQALHHPNLRNLYNYFYDRRIYLYLSEYAPRGELYKELQKSCTFDEQRTATIME 183
DB 171 REVEIQSHLRHPNLRNLYNYFYDRRIYLYLSEYAPRGELYKELQKSCTFDEQRTATIME 230
QY 184 LADALMYCHGKKVTHRDIKPENLLGLKGLKIADFGWSVHAPSRRKTCGTLDYLPPE 243
DB 231 LANALSYCHSKVTHRDIKPENLLGLKGLKIADFGWSVHAPSRRKTCGTLDYLPPE 290
QY 244 MIEGRMHNEKVDLCIGVLCYELLVGNPPESASNETYRRIVKVDLKPSASVPTGAQDL 303
DB 291 MIEGRMHNEKVDLCIGVLCYELLVGNPPESASNETYRRIVKVDLKPSASVPTGAQDL 350
QY 304 ISKLRHNPESRLPLAQSVAHPVWANSRRVLPSPS 338
DB 351 ISRLKHNASQRLTLAEVLEHPWIKANSK--PPT 383

RESULT 20
Q7TNK2 PRELIMINARY; PRT; 395 AA.
ID Q7TNK2 PRELIMINARY; PRT; 395 AA.
AC Q7TNK2; 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase 6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Zhou G., Li W., Yu L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AV336976; AAB16152.1; -;
DR HSSP; O14965; 1OL6
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.


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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 395 AA; 44771 MW; 271DC321221A8DD9 CRC64;

Query Match 59.9%; Score 1084; DB 2; Length 395;
Best Local Similarity 62.7%; Pred. No. 1.3e-70;
Matches 210; Conservative 43; Mismatches 78; Indels 4; Gaps 2;

QY 6 NSYPWPVGRQTAPSGSLSTLPQRLKEPVTTPSALVLMRSNVQPTAAPGQKVMENS--G 63
DB 51 NSQRFVSQAQKLGAGQKPAKQKLPAAASVPRPVSRLNPPQKVEQPAASGNDSEKEQASLQK 110
QY 64 TPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 123
DB 111 TETDKRQWLTEDFDIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 170
QY 124 RETEIQAHLHHPNLRILYNYFYDRRIYLLILEYAPRGELYKELOKSCFTDEORTATIMEE 193
DB 171 REVEIQSHLRHPNLRILYGYFHDATRVYLLILEYAPRGELYKELOKSCFTDEORTATYITE 230
QY 184 LADALMYCHGKVKVTHRDIKPENLLGLGKELKADFGWSVHAPSLRKTMCGLDLYLPP 243
DB 231 LANALSVCHSKRVTHRDIKPENLLGSGELKADFGWSVHAPSLRKTMCGLDLYLPP 290
QY 244 MISGRMNEKVDWCIVGVLGYELLGNPPSPESASHNETYRIVKVDLKPSPASVPTGAQDL 303
DB 291 MIEGRMHDEKVDLWSLVGLCYEFLVGMPPPEAHTYQETVYRISRVSFTFPDFVTEGARDL 350
QY 304 ISKLLRHNSERILPLAQVSHHPVANSRRVLPSS 338
DB 351 ISRLKHNASQRLTAEVLHPHWIKANSSK--PPT 383

RESULT 21
Q8C3H8 PRELIMINARY; PRT; 386 AA.
AC Q8C3H8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
DE library, clone:D830019E15 product:serine/threonine kinase 6, full
DE insert sequence.
GN Name=Stk6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RN [3]
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).

QY 6 NSYPWPVGRQTAPSGSLSTLPQRLKEPVTTPSALVLMRSNVQPTAAPGQKVMENS--G 63
DB 51 NSQRFVSQAQKLGAGQKPAKQKLPAAASVPRPVSRLNPPQKVEQPAASGNDSEKEQASLQK 110
QY 64 TPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 123
DB 111 TETDKRQWLTEDFDIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 170
QY 124 RETEIQAHLHHPNLRILYNYFYDRRIYLLILEYAPRGELYKELOKSCFTDEORTATIMEE 193
DB 171 REVEIQSHLRHPNLRILYGYFHDATRVYLLILEYAPRGELYKELOKSCFTDEORTATYITE 230
QY 184 LADALMYCHGKVKVTHRDIKPENLLGLGKELKADFGWSVHAPSLRKTMCGLDLYLPP 243
DB 231 LANALSVCHSKRVTHRDIKPENLLGSGELKADFGWSVHAPSLRKTMCGLDLYLPP 290
QY 244 MISGRMNEKVDWCIVGVLGYELLGNPPSPESASHNETYRIVKVDLKPSPASVPTGAQDL 303
DB 291 MIEGRMHDEKVDLWSLVGLCYEFLVGMPPPEAHTYQETVYRISRVSFTFPDFVTEGARDL 350
QY 304 ISKLLRHNSERILPLAQVSHHPVANSRRVLPSS 338
DB 351 ISRLKHNASQRLTAEVLHPHWIKANSSK--PPT 383

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Heart;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Heart;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Heart;
ADACHI J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AK085861; BAC39557.1; -.
HSSP; O14965; IOL6.
MGD; MGI:894678; Stk6.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_kinase.
InterPro; IPR008271; Ser_thr_kinase.
Pfam; PF00069; Kinase; 1.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 43968 MW; 31970B9CDE31C6A7 CRC64;

Query Match 59.7%; Score 1080; DB 2; Length 386;
Best Local Similarity 63.0%; Pred. No. 2.4e-70;
Matches 208; Conservative 42; Mismatches 78; Indels 2; Gaps 1;

QY 6 NSYPWPVGRQTAPSGSLSTLPQRLKEPVTTPSALVLMRSNVQPTAAPGQKVMENS--G 63
DB 51 NSQRFVSQAQKLGAGQKPAKQKLPAAASVPRPVSRLNPPQKVEQPAASGNDSEKEQASLQK 110
QY 64 TPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 123
DB 111 TETDKRQWLTEDFDIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKGVHQLR 170
QY 124 RETEIQAHLHHPNLRILYNYFYDRRIYLLILEYAPRGELYKELOKSCFTDEORTATIMEE 193
DB 171 REVEIQSHLRHPNLRILYGYFHDATRVYLLILEYAPRGELYKELOKSCFTDEORTATYITE 230
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QY 184 LADALMYCHGKVIHRDIKPNLLGLKGELKIADFGWSVHAPSLRRKTCWGTLDYLPPE 243
DB 231 LANALSYCHSKRVIHRDIKPNLLGLSGELKIADFGWSVHAPSSRRITTCWGTLDYLPPE 290
QY 244 MIEGRMHNEKVDLWCITGVLCYELLVGNPPFPESASHNETVRRIVKVDLKPFPASVPTGAQDL 303
DB 291 MIEGRMHDEKVDLWSLGVLCYELVGMPPFEAHTYQETVRRISRVETFTFDFVTEGARDL 350
QY 304 ISKLLRHNPSERLPLAQVSAHPWVRANSRR 333
DB 351 ISRLKHNASQRITLAEVLEHPWIKANSKK 380

RESULT 22
Q8BP87 PRELIMINARY; PRT; 395 AA.
AC Q8BP87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:5730433106 product:serine/threonine kinase 6, full
DE insert sequence.
GN Name=Stk6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";

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Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Kimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaakawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/Genbank/DDJB databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK077513; BAC36838.1; -.
DR HSSP; O14965; IOL6.
DR MGD; MGI:894678; Stk6.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 395 AA; 44813 MW; 3B081DFE3DC52667 CRC64;

Query Match 59.3%; Score 1073; DB 2; Length 395;
Best Local Similarity 62.1%; Pred. No. 7,9e-70;
Matches 208; Conservative 43; Mismatches 80; Indels 4; Gaps 2;

QY 6 NSVPWPYQGTAPSGLSLTPQRLKRPVTPSALVMSRSNVQPTAAPQCKVWNS--G 63
DB 51 NSQRPVSQAQKLGAGKAPKAPKOLPAASVPRVSRLLNPNQNEQPAASGNDSEKQASLQK 110
QY 64 TPDILTRHFTIDDFEIGRLGKGFNVLAREKSHFTVALKVLKFSQIEKEGVHQLR 123
DB 111 TEDTKRQWLTSEDFDIGRLGKGFNVLAREKSHFTVALKVLKFSQIEKEGVHQLR 170
QY 124 REIEIQALHHPNLRNLVNYFYDRRIYLIILEYAPRGELYKELQKSCCTFDEQRTATIMEE 183
DB 171 REVEIQSHLRHPNLRNLVNYFYDRRIYLIILEYAPRGELYKELQKSCCTFDEQRTATIMEE 230
QY 184 LADALMYCHGKVIHRDIKPNLLGLKGELKIADFGWSVHAPSLRRKTCWGTLDYLPPE 243
DB 231 LANALSYCHSKRVIHRDIKPNLLGLSGELKIADFGWSVHAPSSRRITTCWGTLDYLPPE 290
QY 244 MIEGRMHNEKVDLWCITGVLCYELLVGNPPFPESASHNETVRRIVKVDLKPFPASVPTGAQDL 303
DB 291 MIEGRMHDEKVDLWSLGVLCYELVGMPPFEAHTYQETVRRISRVETFTFDFVTEGARDL 350
QY 304 ISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSP 338
DB 351 ISRLKHNASQRITLAEVLEHPWIKANSKK--PPT 383

RESULT 23
STK6 RAT
ID STK6 RAT STANDARD; PRT; 397 AA.
AC P59241;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Aurora-A) (ratAurA).
GN Name=Stk6; Synonyms=Stk15;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar Furth; TISSUE=Mammary gland;
RX MEDLINE=22119444; PubMed=12124350;
RA Geopfert T.M., Adigun Y.E., Zhong L., Gay J., Medina D.,
RA Brinkley W.R.;
RT "Centrosome amplification and overexpression of aurora A are early
RT events in rat mammary carcinogenesis.";
RL Cancer Res. 62:4115-4122(2002).
RN [2]
RP MEDLINE=21306577; PubMed=11413462; DOI=10.1038/35048096;
RX Nigg E.A.;
RA "Mitotic kinases as regulators of cell division and its checkpoints.";
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
CC and/or telophase, in relation to the function of the
CC centrosome/spindle pole region during chromosome segregation. May
CC maybe involved in microtubule formation and/or stabilization. May
CC play a key role during tumor development and progression.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
CC and at each spindle pole in mitosis (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in mammary gland and tumor.
CC -!- INDUCTION: Activated by progesterone.
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF537333; AA06823.1; -
CC HSSP; P31751; IGZK.
CC RGD; 628895; Stk6.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc_1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Cell cycle; Phosphorylation;
CC Serine/threonine-protein kinase; Transferase.
FT DOMAIN 126 376 Protein kinase.
FT NP_BIND 132 140 ATP (By similarity).
FT BINDING 155 155 ATP (By similarity).
FT ACT_SITE 249 249 Proton acceptor (By similarity).
SQ SEQUENCE 397 AA; 44874 MW; 95DECA2198DCED85 CRC64;
Query Match 59.2%; Score 1071; DB 1; Length 397;
Best Local Similarity 60.8%; Pred. No. 1.1e-69;
Matches 211; Conservative 39; Mismatches 77; Indels 20; Gaps 3;
QY 14 RQTAPGSLSPKOR-----VLRKEVPTPSALVMSRSNVQPTAAPGQKVMENSS- 62
DB 45 RVLCPNSQVRPQAKPQVAGKPLVQLPAAAGPRPASRLSNPQKSEQPQPAASGNSE 104
QY 63 -----GTPDIITRHTIDDFRGLRGLGKFGNVLAREKKSHFIVALKVLFKSQIEK 115

Db 105 KQOTSQKTEDESKQWLTDFDGRPLGKGFNGVILAREKQSKILLKVLFRKQLEK 164
QY 116 EGVHQLRREIRIQAHLHPNLRILNRYFYDRRRYLIILEYAPRGELYKELQSKCTFDEQ 175
DB 165 AGVEHQLRREVEIQSHLRHPNLRILNRYFYDFHATRVVLIILEYAPLGTVYRELQKLSKDFEQ 224
QY 176 RTATIMEELADALMYCHGKVKVHRDIKPNLLILGLGKELKIADFGVSHVAPSLRRRTMCG 235
DB 225 RTATYITELANALSYCHSRVHRDIKPNLLILGSGELKIADFGVSHVAPSSRRRTTLCG 284
QY 236 TLDYLPPEMIEGRMNEKVDLCIGVLCYELAVGNPPESASHNETYRRIVKVDLKFPPAS 295
DB 285 TLDYQPEMIEGRMDEKVDLWSLGVLCYEFVGMPPFEAHTYQETIRISRVEFTFPDF 344
QY 296 VPTGAQDLISKLRHNPSELELAQVSAHPVWRANSRRVLPSPALOS 342
DB 345 VTGARDLLISRLKKNSSQRLTAEVLEHPWIKANSSK--PPTGHNS 389
RESULT 24
ST6L XENLA
ID ST6L XENLA STANDARD; PRT; 408 AA.
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Eg2-like (EC 2.7.1.37) (p46X1Bg22).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eggs;
RA Roghi C., le Guellac R., Paris J., Couturier A., Philippe M.;
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z17206; CAA78914.1; ALT_INIT.
CC HSSP; P06244; 1FOT.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_Thr_pkin_AS.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc_1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; Cell cycle; Phosphorylation;
CC Serine/threonine-protein kinase; Transferase.
FT DOMAIN 140 390 Protein kinase.
FT NP_BIND 146 154 ATP (By similarity).
FT

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FT BINDING 169 169 ATP (By similarity).
FT ACT SITE 263 263 Proton acceptor (By similarity).
SQ SEQUENCE 408 AA; 46461 MW; 97F6A69C7357AE8 CRC64;

Query Match 58.7%; Score 1062; DB 1; Length 408;
Best Local Similarity 59.8%; Pred. No. 5.2e-69;
Matches 207; Conservative 44; Mismatches 63; Indels 32; Gaps 4;

QY 20 GLSTLPQRLV--RKEPV-----TPSALVLM-----SRSNVQPTAAPGQKV 57
Db 51 GPSNVQFQVMQAKPVLNSQKPTAGLLRPATHGHQTSKPGQPNRNRPQQTSHSSTPN 110
QY 58 MENSSTGTPDILT-----RHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKV 107
Db 111 MEKKGSTDQKTLAVPKESGKKQWCLEDFEIGRPLGKGFNGVYLAREKKSHFIVALKV 170
QY 108 LFKSQLEKGEVHQLRRETEIOAHLHPNLRILNYFYDRRRIYLLILEVAPRGELYKEIQ 167
Db 171 LFKSQLEKAGVEHQLRREVEIOSHLRHPNLRILNYGYFHDASRYLLILDYAPGGELFRELQ 230
QY 168 KSCTFDEQRTATIMEELADALMYCHGKVKVHRDIKPEINLLGLGKELKIADFGWSVHAPS 227
Db 231 KCTRFDDQRSALYIKQALAEALLYCHSKKVIHRDIKPEINLLGNSGELKIADFGWSVHAPS 290
QY 228 LRKRTKMGTLDYLPPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYK 287
Db 291 SRTTLCGTLGYLPPMIEGRMNEKVDLWSLGVLCYELLVGNPPFETDTHQETYRRIK 350
QY 288 VDLKFPASVPTGAQDLISKLLRNPSERLPLAQSHPWVRANSRR 333
Db 351 VEFQPPYVSEAKDLVSKLLKHNPHRLPLKGVLEHPWIVKNSQ 396

RESULT 25
Q6DUK0 PRELIMINARY; PRT; 408 AA.
ID Q6DUK0
AC Q6DUK0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC398349 protein.
GN Xenopus laevis (African clawed frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC075177; AAH75177.1; -.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P-protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 408 AA; 46477 MW; FD4855CC6708E5E7 CRC64;

Query Match 58.6%; Score 1060; DB 2; Length 408;
Best Local Similarity 59.8%; Pred. No. 7.2e-69;
Matches 207; Conservative 44; Mismatches 63; Indels 32; Gaps 4;

QY 20 GLSTLPQRLV--RKEPV-----TPSALVLM-----SRSNVQPTAAPGQKV 57
Db 51 GPSNVQFQVMQAKPVLNSQKPTAGLLRPATHGHQTSKPGQPNRNRPQQTSHSSTPN 110
QY 58 MENSSTGTPDILT-----RHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKV 107
Db 111 MEKKGSTDQKTLAVPKESGKKQWCLEDFEIGRPLGKGFNGVYLAREKKSHFIVALKV 170
QY 108 LFKSQLEKGEVHQLRRETEIOAHLHPNLRILNYFYDRRRIYLLILEVAPRGELYKEIQ 167
Db 171 LFKSQLEKAGVEHQLRREVEIOSHLRHPNLRILNYGYFHDACRYLLILDYAPGGELFRELQ 230
QY 168 KSCTFDEQRTATIMEELADALMYCHGKVKVHRDIKPEINLLGLGKELKIADFGWSVHAPS 227
Db 231 KCTRFDDQRSALYIKQALAEALLYCHSKKVIHRDIKPEINLLGNSGELKIADFGWSVHAPS 290
QY 228 LRKRTKMGTLDYLPPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYK 287
Db 291 SRTTLCGTLGYLPPMIEGRMNEKVDLWSLGVLCYELLVGNPPFETDTHQETYRRIK 350
QY 288 VDLKFPASVPTGAQDLISKLLRNPSERLPLAQSHPWVRANSRR 333
Db 351 VEFQPPYVSEAKDLVSKLLKHNPHRLPLKGVLEHPWIVKNSQ 396

RESULT 26
STK6_HUMAN STANDARD; PRT; 403 AA.
ID STK6_HUMAN
AC Q14865; O60445; O75873; Q980D6; Q9UGG5;
DT 28-FEB-2003 (Ref. 41, Created)
DT 28-FEB-2003 (Ref. 41, Last sequence update)
DT 25-OCT-2004 (Ref. 45, Last annotation update)
DE Serine/threonine-protein kinase 6 (EC 2.7.1.37) (Serine/threonine
DE kinase 15) (Aurora/PL1-related kinase 1) (Aurora-related kinase 1)
DE (HARK1) (Aurora-A) (Breast-tumor-amplified kinase).
GN Name=STK6; Synonyms=AiK, ARK1, AURA, BTAK, STK15;
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OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Blood;
 RX MEDLINE=97298083; PubMed=9153231; DOI=10.1074/jbc.272.21.13766;
 RA Kimura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
 RA Okano Y.;
 RT "Cell cycle-dependent expression and spindle pole localization of a
 RT novel human protein kinase, Aik, related to Aurora of Drosophila and
 RT yeast Ipl1.";
 RL J. Biol. Chem. 272:13766-13771(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98183439; PubMed=9514916; DOI=10.1006/bbrc.1998.8250;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2.";
 RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Breast;
 RX MEDLINE=98442657; PubMed=9771714; DOI=10.1038/2496;
 RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
 RA Brinkley B.R., Sen S.;
 RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
 RT aneuploidy and transformation.";
 RL Nat. Genet. 20:189-193(1998).
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Wang L., Thibodeau S.N.;
 RT "Mutational analysis of the STK15 gene in human tumors.";
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehesvahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Swann R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Cervix, Colon, Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RN CELL-CYCLE REGULATION.
 RP MEDLINE=2195866; PubMed=11790771; DOI=10.1074/jbc.M108252200;
 RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
 RA Ishigatsubo Y.;
 RT "Cell-cycle-dependent regulation of human aurora A transcription is
 RT mediated by periodic repression of E4TF1.";
 RL J. Biol. Chem. 277:10719-10726(2002).
 RN [8]
 RN REVIEW.
 RP MEDLINE=21306577; PubMed=11413462; DOI=10.1038/35048096;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
 CC and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC Maybe involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 CC skeletal muscle, thymus and spleen. Also highly expressed in
 CC colon, ovarian, prostate, neuroblastoma, breast and cervical
 CC cancer cell lines. Expression is cell-cycle regulated, low in
 CC G1/S, accumulates during G2/M, and decreases rapidly after.
 CC -!- PTM: Phosphorylated.
 CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome
 CC aberrations including aneuploidy.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. Aurora
 CC subfamily.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in positions 105, 125, 129, 235 and 241.
 CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
 CC different proteins, it is clear that they are the same protein.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D84212; BAA23592.1; ALT FRAME.
 CC EMBL; AF008551; AAC12708.1; -
 CC EMBL; AF011467; AAC23448.1; -
 CC EMBL; AF011468; AAC63902.1; -
 CC EMBL; AF195947; AAF29508.1; -
 CC EMBL; AF195942; AAF29508.1; JOINED.
 CC EMBL; AF195943; AAF29508.1; JOINED.
 CC EMBL; AF195944; AAF29508.1; JOINED.
 CC EMBL; AF195945; AAF29508.1; JOINED.
 CC EMBL; AF195946; AAF29508.1; JOINED.


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Qy 89 GNVYLAREKSHPIVALKVLFSQIEKEGVEHQLRRIETQAHILHNPILRLNYFYDRR 148
Db 152 GNVYLARESKFTLALKVLFSQIEKEGVEHQLRRIETQAHILHNPILRLNYFYDAS 211
Qy 149 RIVYLIVAPRGELYKELOKSCFTDEORTATIMEELADALMYCHGKVIHRDIPENLL 208
Db 212 RVYLIDYAPGGLFRELQKCTREDDORSAMYIKQALAEALLYCHSKVIRHDIPENLL 271
Qy 209 GLKGBELKIADFGSVHAPSARRKTMCTGLDYLPPEMIEGRMNEKVDLWCIGVLYCYELLV 268
Db 272 GSNGLKIADFGSVHAPSARRKTMCTGLDYLPPEMIEGRMNEKVDLWSLGLVLYCYEFLV 331
Qy 269 GNPFFESASHNETYRRIVKVDLKPASVPTGCAQDLISKILRHNPSERLPLAQVSAHPWR 328
Db 332 GKPPFFEDTHQETYYRIRISKVEFYPPYVSEARDLVSKLKHNPNNHRLPLKGVLEHPWII 391
Qy 329 ANSR 332
Db 392 KNSQ 395

RESULT 28
Q6DBZ4 PRELIMINARY; PRT; 405 AA.
AC Q6DBZ4; 2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zgc:100912 protein.
GN Name=zgc:100912;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC078304; AAH78304.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein-tyrosine kinase activity; IEA.
DR InterPro: IPR011009; Kinase-like.
DR InterPro: IPR000468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.

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DR InterPro: IPR008271; Ser_thr_kin_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; T_YKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 405 AA; 45447 MW; B04793FC827BD489 CRC64;

Query Match 57.6%; Score 1041.5; DB 2; Length 405;
Best Local Similarity 58.4%; Pred. No. 1.6e-67;
Matches 195; Conservative 49; Mismatches 79; Indels 11; Gaps 2;

Qy 11 PYGRQTAPSGLSLTLPOR---VLRKEPVTSPALVMSRSNVQP-----TAAPGQKVM 59
Db 61 PVGKTSQCPGDQNTREPHQKPAHSKQPKPLSAETNKTAEPSKQDKPHQTPSTSTSS 120
Qy 60 NSSGTPDIILTRHFTIDDFEIGRLPGKGFQNVYLAREKSHFIVALKVLFKSQIEKEGVE 119
Db 121 NTSSGSSKSKKAWTLENFDIGRALGKGFQSVYLAREQQTFFILALKVLFKQLEKAGVE 180
Qy 120 HQLRREIEIQAHILHNPILRLNYFYDRIIRYIILYAPRGELYKELOKSCFTDEORTAT 179
Db 181 HQLRREIEIQSHLRHNPILRLNYFYDRIIRYIILYAPRGELYKELOKSCFTDEORTAT 240
Qy 180 IMEELADALMYCHGKVIHRDIPENLLGLKGLKELIADFGSVHAPSARRKTMCGTLDY 239
Db 241 YIMELADALRYCHSKAVIHRDIPENLLGLKGLKELIADFGSVHAPSARRKTMCGTLDY 300
Qy 240 LPPEMIEGRMNEKVDLWCIGVLYCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTG 299
Db 301 LPPEMIEGTHDEKVDLWSLGLVLYCYEFLVGRPPFETKSHETRYKISRVEFTYPAHVSNG 360
Qy 300 AQDLISKILRHNPSERLPLAQVSAHPWRANSRR 333
Db 361 SRDLINRLKHNPMHRLPIQGVMEHPWVVENSTK 394

RESULT 29
Q9M077 PRELIMINARY; PRT; 294 AA.
AC Q9M077;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative serine/threonine protein kinase.
GN Name=AT4g32830;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AL161582; CAB80000.1; -.
DR PIR: T10690; T10690.
DR HSSP: O14965; 1OL6.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase-like.
DR InterPro: IPR002290; Ser_thr_kinase.

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DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser Thr kinase.
DR InterPro: IPR008271; Ser Thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 294 AA; 33972 MW; B6669E1799083BE4 CRC64;

Query Match 52.0%; Score 940; DB 2; Length 294;
Best Local Similarity 60.3%; Pred. No. 2.6e-60;
Matches 179; Conservative 47; Mismatches 63; Indels 8; Gaps 4;

QY 49 PTAAPQKQWNSGTPDILTRHFTIDDFEIGRLPGKFGNVLAREKSHFIVALKVL 108
Db 4 PTETQHQE-KEASDASAAAAQKRWTLSDFDIGKPLGRGKFGHVLAREKSNHVALKVL 62
QY 109 FKSQIEKEGVHQLRREIEIQAHLPNLRILNYFYDRRIYLLILEYAPRGELYKELOK 168
Db 63 FKSQSQSQVQEHQRLREVEIQSHLRPNILRLGYFDQKRVYLILLEYAARGELYKDLOK 122
QY 169 SCTFDQRTATIMEELADALMYCHGKKVIHRDIKPENLLILGLKGLKIADFGWSVHAPSL 228
Db 123 CKYFSERRAATYVASLARALYCHGKHVIHRDIKPENLLIGAQGLKIADFGWSVHTFN- 181
QY 229 RRTMCTGTLDPPEMIEGRMNEKVDLWCIGVLYCELLVGNPPPSASGHNETYRIRVKV 288
Db 182 RRTMCTGTLDPPEMVESVEHDASVDIWSGLICLYEFYGVPPFPEAMEHSDTYRIRVQV 241
QY 289 DLKFPAS--VPTCAQDLISKLRHNPSERLPLAQVSAHPWVRNSRRVLPSPALQSV 343
Db 242 DLKFPKPKPIISAKOLLISQMLVKESQRLPLHLKLEHPWVQNA----DPSCIYRV 294

RESULT 30
Q8LXB4 PRELIMINARY; PRT; 294 AA.
AC Q8LXB4
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative serine/threonine protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY086942; AAM64506.1; -.
DR HSSP; O14965; 1OL6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase-like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser Thr_pkinase.
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DR InterPro: IPR008271; Ser Thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 294 AA; 33926 MW; E1D048CCF4BEED3F CRC64;

Query Match 51.8%; Score 937; DB 2; Length 294;
Best Local Similarity 60.3%; Pred. No. 4.2e-60;
Matches 179; Conservative 46; Mismatches 64; Indels 8; Gaps 4;

QY 49 PTAAPQKQWNSGTPDILTRHFTIDDFEIGRLPGKFGNVLAREKSHFIVALKVL 108
Db 4 PTETQHQE-KEASDASAAAAQKRWTLSDFDIGKPLGRGKFGHVLAREKSNHVALKVL 62
QY 109 FKSQIEKEGVHQLRREIEIQAHLPNLRILNYFYDRRIYLLILEYAPRGELYKELOK 168
Db 63 FKSQSQSQVQEHQRLREVEIQSHLRPNILRLGYFDQKRVYLILLEYAARGELYKDLOK 122
QY 169 SCTFDQRTATIMEELADALMYCHGKKVIHRDIKPENLLILGLKGLKIADFGWSVHAPSL 228
Db 123 CKYFSERRAATYVASLARALYCHGKHVIHRDIKPENLLIGAQGLKIADFGWSVHTFN- 182
QY 229 RRTMCTGTLDPPEMIEGRMNEKVDLWCIGVLYCELLVGNPPPSASGHNETYRIRVKV 288
Db 183 RR-TMCTGTLDPPEMVESVEHDASVDIWSGLICLYEFYGVPPFPEAMEHSDTYRIRVQV 241
QY 289 DLKFPAS--VPTCAQDLISKLRHNPSERLPLAQVSAHPWVRNSRRVLPSPALQSV 343
Db 242 DLKFPKPKPIISAKOLLISQMLVKESQRLPLHLKLEHPWVQNA----DPSCIYRV 294

RESULT 31
O82309 PRELIMINARY; PRT; 282 AA.
AC O82309
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein At2g25880.
GN Names=At2g25880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Rønning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Carninci P., Hayashizaki Y.,
RA Ishida J., Kamiya A., Kawai J., Narusaka M., Sakurai T., Satou M.,
RA Seki M., Shinozaki K., Ecker J.R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AC005395; AAC42257.1; -.
DR EMBL; BT010653; AAR07517.1; -.
DR PIR; H84653; H84653.
DR HSSP; O14965; 1OL6.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser Thr_pkinase.
```


[illegible]

KW Hypothetical protein.
SQ SEQUENCE 288 AA; 33310 MW; 732F036B2E707909 CRC64;

Query Match 50.9%; Score 921.5; DB 2; Length 288;
Best Local Similarity 63.7%; Pred. No. 5.4e-59;
Matches 174; Conservative 42; Mismatches 50; Indels 7; Gaps 3;

QY 70 RHTTIDDFEIGPLGKGFNVYLAREKKSHFIIVALKVLFKSQIEKEGVHQLRREIQT 129
:
Db 18 KRWTTSDFDIGPLGRKGFGHYLAREKSRDHIVALKVLFKAQQSOQVEHQLRREIQT 77

QY 130 AHLHPNIIRLNYFYDRRIILLEYAPRGELYKELOKSTCFDQRATIMEELADALM 189
:
Db 78 SHLRHPNIIRLNYGYFYDKRVVLILEYAVRGELYKELOKCYFSERRAATVVASLARALI 137

QY 190 YCHGKVVIHRDIKPENLLGLKGELKIADFGWSHVAPSRLRTKTCGTLDLYLPPEMIEGRM 249
:
Db 138 YCHGKHVIHRDIKPENLLIGAOGELKIADFGWSVHTFN--RRRTMGCTLDLYLPPEMVESVE 196

QY 250 HNEKVDLMICIGVLCYELLVGNPPPSASHNETYRIRVKVDLKFPAS--VPTGAODLISKL 307
:
Db 197 HDASVDINSIGLICVEFLYGVPFFEARHSEYTKRIVQVDLKFPKPIVSSAKDLISQM 256

QY 308 LRHPNSERILPQAQSAHPVNRANSRRLVPPSAL 340
:
Db 257 LVKESTQRLAHKLLEHPWVQNA----DPSGL 285

RESULT 33
Q9LG71 PRELIMINARY; PRT; 432 AA.

ID AC Q9LG71; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0710E05.26 (Hypothetical protein P0671B11.2).
GN Names=P0710E05.26; Synonyms=P0671B11.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947; [1]
RN RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Wu J., Nilimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idenuma A., Iijima M., Ikeda M., Ikeno M., Itoh S., Itoh T., Itoh Y., Ito H., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., Kamekura K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y., Nakaseki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saiji S., Sakai K., Shibata M., Shinokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Xano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF002743; BAA99439.1; --
DR EMBL; AP002746; BAB2687.1; --
DR FSPS; O14965; IOL6.
DR Gramene; Q9LG71; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPRO11009; Kinase_like.
DR InterPro; IPRO00719; Prot kinase.
DR InterPro; IPRO2290; Ser thr pkinae.

InterPro; IPRO11009; Kinase_like.
InterPro; IPRO00719; Prot kinase.
Pfam; PF00069; Pkinase; 1.
ProDom; PD00001; Proteinkinase_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00111; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
KW ATP-binding; Hypothetical protein; Kinase;
Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 282 AA; 32757 MW; 3475F9C04D168B7E CRC64;

Query Match 50.9%; Score 921.5; DB 2; Length 282;
Best Local Similarity 63.7%; Pred. No. 5.4e-59;
Matches 174; Conservative 42; Mismatches 50; Indels 7; Gaps 3;

QY 70 RHTTIDDFEIGPLGKGFNVYLAREKKSHFIIVALKVLFKSQIEKEGVHQLRREIQT 129
:
Db 12 KRWTTSDFDIGPLGRKGFGHYLAREKSRDHIVALKVLFKAQQSOQVEHQLRREIQT 71

QY 130 AHLHPNIIRLNYFYDRRIILLEYAPRGELYKELOKSTCFDQRATIMEELADALM 189
:
Db 72 SHLRHPNIIRLNYGYFYDKRVVLILEYAVRGELYKELOKCYFSERRAATVVASLARALI 131

QY 190 YCHGKVVIHRDIKPENLLGLKGELKIADFGWSHVAPSRLRTKTCGTLDLYLPPEMIEGRM 249
: : : : ~~~~~~ :
Db 132 YCHGKHVIHRDIKPENLLIGAOGELKIADFGWSVHTFN--RRRTMGCTLDLYLPPEMVESVE 190

QY 250 HNEKVDLMICIGVLCYELLVGNPPPSASHNETYRIRVKVDLKFPAS--VPTGAODLISKL 307
:
Db 191 HDASVDINSIGLICVEFLYGVPFFEARHSEYTKRIVQVDLKFPKPIVSSAKDLISQM 250

QY 308 LRHPNSERILPQAQSAHPVNRANSRRLVPPSAL 340
:
Db 251 LVKESTQRLAHKLLEHPWVQNA----DPSGL 279

RESULT 32
Q683C9 PRELIMINARY; PRT; 288 AA.

ID AC Q683C9; 25-OCT-2004 (TrEMBLrel. 28, Created)
DT DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein At2g25880.
GN Names=At2g25880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702; [1]
RN RP SEQUENCE FROM N.A.
RX Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyota T., Konagaya A., Carninci P., Kawai J., Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAPL) cDNAs.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK15188; BAD42951.1; --
DR InterPro; IPRO11009; Kinase like.
DR InterPro; IPRO00719; Prot kinase.
DR InterPro; IPRO2290; Ser thr pkinae.
DR InterPro; IPRO08271; Ser thr pkinae.
DR InterPro; IPRO01245; Tyr_pkinae.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD00001; Proteinkinase; 1.
DR SMART; SM00220; S TKC; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:46:50 ; Search time 143.505 Seconds
(without alignments)
1086.128 Million cell updates/sec

Title: US-10-734-126-4

Perfect score: 2110

Sequence: 1 MBRSKNCISGPKATAPVG.....TANSSKPSNCQKESASKQS 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%

Maximum Match 100%

Listing first 65000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2110	100.0	403	2 AAW18084	Aaw18084 Human Aur
2	2110	100.0	403	2 AAY22476	Aay22476 Human Aur
3	2110	100.0	420	5 ABP41958	Abp41958 Human ova
4	2109	100.0	403	4 AAG67614	Aag67614 Amino aci
5	2109	100.0	403	4 AAG67435	Aag67435 Amino aci
6	2109	100.0	403	7 ADF61840	Adf61840 Human ser
7	2109	100.0	403	8 ADQ89832	Adq89832 Antagonis
8	2109	100.0	403	8 ADR05174	Adr05174 Human GTP
9	2104	99.7	403	6 ABP97367	Abp97367 Human bla
10	2104	99.7	403	6 ABR48160	Abp97367 Human bla
11	2104	99.7	403	7 ADN39888	Adn39888 Cancer/an
12	2104	99.7	403	8 ADE15337	Adel5337 Truncated
13	2104	99.7	403	8 ADH59556	Adh59556 Monoclonal
14	2104	99.7	403	8 ADM72205	Adm72205 Human mod
15	2104	99.7	403	8 ADM72205	Adm72205 Human TAS
16	2103	99.7	403	6 ABP97366	Abp97366 Human ser
17	2095	99.3	403	7 ADJ31727	Adj31727 Human mit
18	1935.5	91.7	402	7 ABR61579	Abp97366 Human ser
19	1935.5	91.7	402	7 ABR61579	Abp97366 Human ser
20	1924	91.2	403	5 AAO18740	Aao18740 Human NOV
21	1614	76.5	319	6 ABP97470	Abp97470 Truncated
22	1503	71.2	309	6 ABP97472	Abp97472 Truncated
23	1460	69.2	300	6 ABP97473	Abp97473 Truncated
24	1215	57.6	248	8 ADK71858	Adk71858 Human kin
25	1057.5	50.1	344	2 AAW18083	Aaw18083 Human Aur

26	1057.5	50.1	344	2 AAY22475	Aay22475 Human Aur
27	1057.5	50.1	344	4 AAG67615	Aag67615 Amino aci
28	1057.5	50.1	344	4 AAG67436	Aag67436 Amino aci
29	1057.5	50.1	344	6 ABR48188	Abp41958 Human ova
30	1057.5	50.1	344	6 ABUS6641	Abu56641 Lung canc
31	1057.5	50.1	344	6 ABR92152	Abp92152 Human cer
32	1057.5	50.1	344	7 ADB80537	Adb80537 Ovarian c
33	1057.5	50.1	344	7 ADN38885	Adn38885 Cancer/an
34	1057.5	50.1	344	7 ADN95464	Adn95464 Human BEC
35	1057.5	50.1	344	8 ADK67718	Adk67718 Human mod
36	1057.5	50.1	344	8 ADQ89834	Adq89834 Antagonis
37	1057.5	50.1	344	8 ABM81826	Abm81826 Tumour-as
38	1056.5	50.1	344	7 ABR61580	Abp61580 Human HSA
39	1050	49.8	343	2 AAW99783	Aaw99783 Rac AIM-1
40	1046	49.6	347	2 AAY27052	Aay27052 Human pro
41	1046	49.6	347	6 ABUS7643	Abu57643 Different
42	1045	49.5	320	8 ADOS7331	Ado57331 Kidney de

ALIGNMENTS

RESULT 1

AAW18084
ID AAW18084 standard; protein; 403 AA.

AC AAW18084;

XX 07-SEP-1997 (first entry)

XX Human Aurora-2.

XX Auroxa-2; AUR-2; signal transduction; protein kinase; tumour; cancer;
protein kinase; gene therapy; diagnosis; antibody.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..130

FT /label= N-terminal_domain

FT Misc-difference 50 /note= "deduced residue from some cDNA clones is Leu"

FT Misc-difference 50 /note= "deduced residue from some cDNA clones is Leu"

FT Misc-difference 57 /note= "deduced residue from some cDNA clones is Ile"

FT Misc-difference 57 /note= "deduced residue from some cDNA clones is Ile"

FT Misc-difference 57 /note= "deduced residue from some cDNA clones is Ile"

FT Domain 131..403

FT /label= Kinase_domain

FT Modified-site 288

FT /label= Phosphorylation

FT /note= "cAMP-dependent protein kinase phosphorylation site conserved in AUR-2 and yeast and Drosophila homologues"

FT Modified-site 334

FT /label= Phosphorylation

FT /note= "tyrosine phosphorylation consensus site conserved in Drosophila aurora but not in AUR-1 or yeast IPL1"

FT Modified-site 342

FT /label= Phosphorylation

FT /note= "cAMP-dependent protein kinase phosphorylation site conserved in AUR-2 and yeast and Drosophila homologues"

WO9722702-A1.

26-JUN-1997.

25-NOV-1996;

19-DEC-1995;

14-AUG-1996;

96WO-US018859.

95US-0008809P.

96US-00023943P.

XX	ABP41958 standard; protein; 420 AA.	SQ	Sequence 420 AA;	
AC	ABP41958;		Query Match	100.0%; Score 2110; DB 5; Length 420;
XX			Best Local Similarity	100.0%; Pred. No. 1e-186;
DT	22-AUG-2002 (first entry)		Matches	403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX				
DE	Human ovarian antigen HPCOK03, SEQ ID NO:3090.	QY	1	MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVSNGQARVLCPSNSSQRVPLQ 60
XX				
XX	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;	DB	18	MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVSNGQARVLCPSNSSQRVPLQ 77
KW	ovarian cancer; breast cancer; tumour; reproductive system disorder;			
KW	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;	QY	61	AQKLVSCHKVQKQKQLOCATSVPHVPSRPLNNTQSKOPLPSAPENNPEELASKQKN 120
KW	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;	DB	78	AQKLVSCHKVQKQKQLOCATSVPHVPSRPLNNTQSKOPLPSAPENNPEELASKQKN 137
KW	inflammatory condition; immune disorder; blood disorder;			
KW	cardiovascular disorder; respiratory disorder; neurological disorder;	QY	121	EESKQKQWALEDFEIGRPLGKGFNGVYLLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 180
KW	gastrointestinal disorder; urinary system disorder; drug screening;	DB	138	EESKQKQWALEDFEIGRPLGKGFNGVYLLAREKQSKFIALKVLKFAQLEKAGVEHQLRR 197
KW	gene therapy; chromosome mapping; forensic analysis;			
KW	antibody preparation; cytostatic; immunomodulatory; neuroprotective;	QY	181	EVEIQSHLRHPNLRILYGYFHDATRVYLLIYAPLGTIVYRELQKLSKPFDEQRTATYITEL 240
KW	antiinflammatory; gynaecological; reproductive; chromosome 20q13.2-13.3.	DB	198	EVEIQSHLRHPNLRILYGYFHDATRVYLLIYAPLGTIVYRELQKLSKPFDEQRTATYITEL 257
OS	Homo sapiens.			
XX		QY	241	ANALSYCHSKRVTHRDIKPNLLLGAGELKIADFGWSVHAPSSRRRTTLCGTLIDYLPPEM 300
PN	WO200200677-A1.			
XX		DB	258	ANALSYCHSKRVTHRDIKPNLLLGAGELKIADFGWSVHAPSSRRRTTLCGTLIDYLPPEM 317
XX	03-JAN-2002.			
XX	07-JUN-2001; 2001WO-US018569.	QY	301	IEGRHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETIKRISRVEFTFPDFVTEGARDLI 360
XX	07-JUN-2000; 2000US-0209467P.	DB	318	IEGRHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETIKRISRVEFTFPDFVTEGARDLI 377
XX	(HUMA-) HUMAN GENOME SCI INC.			
XX		QY	361	SRLLKKNPSQRPMLREVLEHPWITANSKPSNCKNESASKQS 403
PI	Birse CE, Rosen CA;	DB	378	SRLLKKNPSQRPMLREVLEHPWITANSKPSNCKNESASKQS 420
XX	WPI; 2002-147878/19.			
DR	N-PSDB; ABQ55035.	RESULT 4		
XX		AAG67614		
XX		ID	AAG67614	standard; protein; 403 AA.
XX		XX	AC	AAG67614;
XX		XX	DT	26-NOV-2001 (first entry)
PS	Claim 11; SEQ ID NO 3090; 2922pp; English.			
XX		DE		Amino acid sequence of a human protein.
CC	The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	KW		Human; protein kinase; protein phosphatase; signal transduction.
CC	encompasses polypeptides 90% identical and polynucleotides 95% identical	XX		Homo sapiens.
CC	to the sequences of the invention. The invention additionally relates to	XX		WO200109316-A1.
CC	recombinant vectors and host cells comprising human ovarian antigen	XX		08-FEB-2001.
CC	polynucleotides, antibodies against human ovarian antigens, and the use	XX		28-JUL-2000; 2000WO-JP005061.
CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,	XX		29-JUL-1999; 99JP-00248036.
CC	treating, prognosing or preventing various ovary and/or breast-related	PR	18-OCT-1999;	99US-0159590P.
CC	disorders. Such conditions include ovarian cancer and breast cancer, and	PR	11-JAN-2000;	2000JP-00118776.
CC	metastatic tumours of ovarian or breast origin, reproductive system	PR	17-FEB-2000;	2000US-0183322P.
CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,	PR	02-MAY-2000;	2000JP-00183767.
CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine	PR	09-JUN-2000;	2000JP-00241899.
CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	XX		(HELI-) HELIX RES INST.
CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	XX		Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
CC	vaginitis), immune disorders (e.g., congenital and acquired	PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;	
CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),	PI	Senoo C, Nezu J;	
CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,	DR	WPI; 2001-570286/64.	
CC	respiratory disorders, neurological disorders, gastrointestinal disorders	XX		New genes encoding proteins with protein kinase/protein phosphatase
CC	and urinary system disorders. Ovarian antigen polypeptides and	PT		activity, useful in the diagnosis and treatment of diseases.
CC	polynucleotides may also be used in screening for compounds which	XX		
CC	modulate ovarian antigen expression or activity. The polynucleotides may			
CC	further be used for gene therapy, chromosome mapping, in the			
CC	identification of individuals and in forensic analysis, and the			
CC	polypeptides may be used as food additives or to prepare antibodies			
CC	useful in disease diagnosis, drug targeting and phenotyping. The present			
CC	sequence represents a human ovarian antigen of the invention. Note: The			
CC	sequence data for this patent did not form part of the printed			
CC	specification, but was obtained in electronic format directly from WIPO			
CC	at ftp.wipo.int/pub/published_pct_sequences			
XX				

KW gastrointestinal; colon cancer; Grave's disease; psoriasis;
KW atherosclerosis; restenosis; vasoproliferative; human;
KW serine/threonine kinase 15; STK15; ARK2; enzyme.

XX Homo sapiens.

XX WO2003088910-A2.

XX 30-OCT-2003.

XX 15-APR-2003; 2003WO-US011867.

XX 15-APR-2002; 2002US-00123568.

XX 15-APR-2002; 2002US-00123731.

XX 16-APR-2002; 2002US-0373366P.

XX (RIGS-) RIGEL PHARM INC.

XX Hitoshi Y, Jenkins Y;

XX WPI; 2003-865396/80.

XX N-PSDB; ADF61839.

XX Identifying a compound that modulates cell cycle arrest, for treating
PT e.g. cancer, comprises contacting a cell comprising a target polypeptide
PT and determining the chemical or phenotypic effect of the compound upon
PT the cell.

XX Claim 1; SEQ ID NO 24; 176pp; English.

XX The invention relates to a novel method for identifying a compound that
CC modulates cell cycle arrest comprising contacting a target polypeptide
CC within a cell with a compound and determining the chemical or phenotypic
CC effect of the compound upon the cell. The method of the invention has
CC cytostatic, antiproliferative, antiarteriosclerotic, vasotropic and
CC antithyroid applications and may be useful for identifying a compound
CC that modulates cell cycle arrest. Such compounds may subsequently be used
CC for developing therapeutic reagents to treat melanoma, breast, ovarian,
CC lung, gastrointestinal or colon cancer, as well as other proliferative
CC diseases such as Grave's disease, psoriasis, atherosclerosis, restenosis
CC and other vasoproliferative diseases. The current sequence is that of the
CC human serine/threonine kinase 15 (STK15;ARK2) protein of the invention.

XX Sequence 403 AA;

Query Match 100.0%; Score 2109; DB 7; Length 403;

Best Local Similarity 99.8%; Pred. No. 1.2e-186;

Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQARVLCPSNSSQRVPLQ 60

DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQARVLCPSNSSQRVPLQ 60

QY 61 AOKLVSSHFPVQKQKQLOATSVHPVSRPLNTOKSKQPLPSAPENPEELASKQKN 120

DB 61 AOKLVSSHFPVQKQKQLOATSVHPVSRPLNTOKSKQPLPSAPENPEELASKQKN 120

QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRR 180

DB 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRR 180

QY 181 EYEQSHLRHNPILRLVGYFHDATRVVLIILEYAPLGTVYRELKLSKFDEQRTATYITEL 240

DB 181 EYEQSHLRHNPILRLVGYFHDATRVVLIILEYAPLGTVYRELKLSKFDEQRTATYITEL 240

QY 241 ANALSYCHSKRVTHRDIKPENLLSGAGELKIADFGWSHAPSSRRTTLCGLDYLPPDM 300

DB 241 ANALSYCHSKRVTHRDIKPENLLSGAGELKIADFGWSHAPSSRRTTLCGLDYLPPDM 300

QY 301 IEGRMDEKVDLWSLGVLCYFELVGKPPPEANTYQETKYKISRVEFTFDFVTEGARDLI 360

DB 301 IEGRMDEKVDLWSLGVLCYFELVGKPPPEANTYQETKYKISRVEFTFDFVTEGARDLI 360

QY 361 SRLLKKNPSQRPMLREVLEHPWITANSSKPSNCKNESASKQS 403
DB 361 SRLLKKNPSQRPMLREVLEHPWITANSSKPSNCKNESASKQS 403

RESULT 7

ADQ89832

ID ADQ89832 standard; protein; 403 AA.

XX ADQ89832;

XX 21-OCT-2004 (first entry)

XX Antagonist of cell cycle progression polypeptide #131.

XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.

XX Homo sapiens.

XX WO2004063362-A2.

XX 29-JUL-2004.

XX 31-DEC-2003; 2003WO-GB005635.

XX 10-JAN-2003; 2003US-0439123P.

XX 06-MAY-2003; 2003US-0468402P.

XX (CYCL-) CYCLACEL LTD.

XX Glover D, Bell G, Frenz L, Midgley C;

XX WPI; 2004-544089/52.

XX N-PSDB; ADQ89831.

XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.

XX Claim 2; SEQ ID NO 262; 461pp; English.

XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.

XX Sequence 403 AA;

Query Match 100.0%; Score 2109; DB 8; Length 403;

Best Local Similarity 99.8%; Pred. No. 1.2e-186;

Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQARVLCPSNSSQRVPLQ 60

DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQARVLCPSNSSQRVPLQ 60

QY 61 AOKLVSSHFPVQKQKQLOATSVHPVSRPLNTOKSKQPLPSAPENPEELASKQKN 120

DB 61 AOKLVSSHFPVQKQKQLOATSVHPVSRPLNTOKSKQPLPSAPENPEELASKQKN 120

QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRR 180

DB 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHQLRR 180

QY 181 EVEIQSHLRHPNLRILYGVFHDTRVYLLEYAPLGTVVYRELQKLSKFDQRTATVITEL 240
DB 181 EVEIQSHLRHPNLRILYGVFHDTRVYLLEYAPLGTVVYRELQKLSKFDQRTATVITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSRRRTTLCGLDYLPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSRRRTTLCGLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYKRISRVETFFDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYKRISRVETFFDFVTEGARDLI 360
QY 361 SRLLEKHPNPSQRPMLREVLEHPWITANSKPSNCKNKESASKOS 403
DB 361 SRLLEKHPNPSQRPMLREVLEHPWITANSKPSNCKNKESASKOS 403

RESULT 8
ADRO5174
ID ADR05174 standard; protein; 403 AA.
XX AC ADR05174;
XX DT 21-OCT-2004 (first entry)
XX Human GTPase regulator-associated w focal adhesion kinase pp125 protein.
DE DE apoptosis; cytosolic; antiinflammatory; antiasthmatic; respiratory;
KW antirheumatic; antiarthritic; gynaecological; cardiant; vasotropic;
KW antipsoriatic; antiulcer; gastrointestinal; immunosuppressive;
KW neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;
KW asthma; chronic obstructive pulmonary disease; cystic fibrosis;
KW rheumatoid arthritis; acute respiratory distress syndrome; preeclampsia;
KW myocardial ischaemia; reperfusion injury; psoriasis; bronchiolitis;
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; human;
KW enzyme; GTPase regulator-associated with focal adhesion kinase pp125;
KW GRAF.
XX Homo sapiens.
XX OS
XX WO2004065959-A2.
XX PN
XX PD 05-AUG-2004.
XX PF 23-JAN-2004; 2004WO-GB000271.
XX PR 23-JAN-2003; 2003GB-00001566.
XX PR 25-MAR-2003; 2003US-0457533P.
XX PA (EIRX-) EIRX THERAPEUTICS LTD.
XX PI Seery L, Hayes I, Murphy F;
XX WPI; 2004-593556/57.
XX DR N-PSDB; ADR05175.
XX PT Identifying a modulator of apoptosis-associated polypeptide function,
PT useful for treating e.g., cancer, comprises incubating a sample
PT containing an apoptosis-associated polypeptide and a candidate agent to
PT permit binding.
XX Claim 1; Page; 230pp; English.
XX The invention relates to a novel method for identifying an agent that
CC modulates the function of an apoptosis-associated polypeptide,
CC particularly a kinase or GPCR (G-protein-coupled receptor). The method
CC comprises providing a sample containing an apoptosis-associated
CC polypeptide and a candidate agent and incubating under conditions to
CC permit binding of the candidate agent to the polypeptide, measuring the
CC binding and comparing it with the binding of the polypeptide to a control
CC agent known not to bind to the polypeptide. The method of the invention
CC has cytostatic, antiinflammatory, antiasthmatic, respiratory,
CC antirheumatic, antiarthritic, gynaecological, cardiant, vasotropic,

CC antipsoriatic, antiulcer, gastrointestinal, immunosuppressive and
CC neuroprotective applications. The method and molecules may be useful for
CC treating a disease or condition characterised by abnormal apoptosis in
CC mammalian tissue, particularly cancer, such as small cell lung cancer,
CC cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,
CC leukaemias, sarcomas and myelomas. Furthermore, autoimmune,
CC neurodegenerative and inflammatory conditions may be treated, including
CC asthma, chronic obstructive pulmonary disease, cystic fibrosis,
CC rheumatoid arthritis, acute respiratory distress syndrome, preeclampsia,
CC myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis,
CC Crohn's disease, ulcerative colitis and inflammatory bowel disease. The
CC current sequence is that of a human apoptosis-associated protein of the
CC invention which was used during siRNA (small interfering RNA)-mediated
CC gene silencing.
XX SQ Sequence 403 AA;
Query Match 100.0%; Score 2109; DB 8; Length 403;
Best Local Similarity 99.8%; Pred. No. 1.2e-186;
Matches 402; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRSKENCISGPKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLIQ 60
DB 1 MDRSKENCISGPKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSSNSQRPVLIQ 60
QY 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
DB 61 AQKLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLSPAPENNPEELASKQKN 120
QY 121 ESKKRQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVFLKQAEKAGVEHQLRR 180
DB 121 ESKKRQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVFLKQAEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNLRILYGVFHDTRVYLLEYAPLGTVVYRELQKLSKFDQRTATVITEL 240
DB 181 EVEIQSHLRHPNLRILYGVFHDTRVYLLEYAPLGTVVYRELQKLSKFDQRTATVITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSRRRTTLCGLDYLPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLGSAGELKIADFGWSVHAPSRRRTTLCGLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYKRISRVETFFDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQTYKRISRVETFFDFVTEGARDLI 360
QY 361 SRLLEKHPNPSQRPMLREVLEHPWITANSKPSNCKNKESASKOS 403
DB 361 SRLLEKHPNPSQRPMLREVLEHPWITANSKPSNCKNKESASKOS 403
RESULT 9
ABP97367
ID ABP97367 standard; protein; 403 AA.
XX AC ABP97367;
XX DT 10-MAY-2003 (first entry)
XX DE Human serine/threonine kinase 15 (STK15), Ile31 variant.
XX Human; serine/threonine kinase 15; STK15; Aurora2; cell cycle;
KW chromosome 20; centrosome-associated kinase; cancer susceptibility;
KW single nucleotide polymorphism; SNP; genetic diagnosis; prognosis;
KW detection; diagnosis; cancer; malignant astrocytoma; glioblastoma;
KW medulloblastoma; gastric cancer; colorectal cancer; colorectal adenoma;
KW acute myelogenous leukaemia; lung cancer; renal cancer; leukaemia;
KW breast cancer; prostate cancer; endometrial cancer; neuroblastoma;
KW enzyme.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX Misc-difference 31
FT

XX Truncated Aurora-2 kinase #SEQ ID 1.
XX Aurora-2 kinase; three dimensional structure; protein co-ordinate data.
XX Homo sapiens.
XX WO2003092607-A2.
XX 13-NOV-2003.
XX 01-MAY-2003; 2003WO-US013605.
XX 01-MAY-2002; 2002US-0377510P.
XX (VERT-) VERTEX PHARM INC.
XX Cheatham G, Knegetel R, Swenson L, Coll JT, Renwick S, Weber P;
XX WPI; 2004-022617/02.
XX Crystal useful for screening, designing and evaluating compounds as
XX agonists or antagonists of Aurora-2 kinases, comprises optionally
XX phosphorylated Aurora-2 kinase domain.
XX Example 1; SEQ ID NO 1; 242pp; English.
XX The invention relates to a crystal comprising an optionally
XX phosphorylated Aurora-2 kinase domain or its homologue. The protein of
XX the invention may be used for identifying agonists or antagonists of
XX Aurora-2 kinases, and for generation of three dimensional structures and
XX structural co-ordinate information of Aurora family proteins. The
XX crystalline structure facilitates the designing of selective inhibitors
XX of Aurora family kinases (particularly Aurora-2 kinase) so that
XX undesirable side effects associated with non-selective inhibitors can be
XX avoided. The structural co-ordinates solve the structure of Aurora-2
XX proteins that have amino acid substitutions, additions and/or mutations,
XX and serve as additional tools to determine the most efficient binding
XX interactions. The current sequence represents the Aurora-2 kinase amino
XX acid sequence.
XX Sequence 403 AA;
XX
XX Query Match 99.7%; Score 2104; DB 8; Length 403;
XX Best Local Similarity 99.8%; Pred. No. 3.5e-186;
XX Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQPPQNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQPPQNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
QY 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENPPEELASKQKN 120
DB 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENPPEELASKQKN 120
QY 121 EESKKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHOLRR 180
DB 121 EESKKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHOLRR 180
QY 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVTVRELOKLSKDFEORTATYTTEL 240
DB 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVTVRELOKLSKDFEORTATYTTEL 240
QY 241 ANALSYCHSKRVTHRIDIKPENLLGSAGELKIAFDGWSVHAPSSRRITLCGLDYLPPPM 300
DB 241 ANALSYCHSKRVTHRIDIKPENLLGSAGELKIAFDGWSVHAPSSRRITLCGLDYLPPPM 300
QY 301 IEGRMDEKVDLSGLVCEFLVGKPPPEANTYQETIKRISRVETFPDFVTEGARDLI 360
DB 301 IEGRMDEKVDLSGLVCEFLVGKPPPEANTYQETIKRISRVETFPDFVTEGARDLI 360
QY 361 SRLKKNPSORPMLREVLEHPWITANSSKPSNCKNESASKQS 403

DB 361 SRLKKNPSORPMLREVLEHPWITANSSKPSNCKNESASKQS 403
XX
XX RESULT 13
XX ADH59556
XX ID ADH59556 standard; protein; 403 AA.
XX AC ADH59556;
XX XX
XX 25-MAR-2004 (first entry)
XX XX
XX Monoclonal antibody of the invention.
XX KW Monoclonal antibody; MAb; aurora-A kinase; Cytostatic.
XX OS Homo sapiens.
XX PN WO2003106500-A1.
XX PD 24-DEC-2003.
XX 12-JUN-2003; 2003WO-FR001772.
XX PF 12-JUN-2002; 2002FR-00007212.
XX PR (CNRS) CENT NAT RECH SCI.
XX PA (FRSA-) ETAB FR DU SANG-BRETAGNE.
XX XX Prigent C, Martin A;
XX WPI; 2004-071550/07.
XX DR N-PSDB; ADH59555.
XX XX New monoclonal antibody specific for aurora-A kinase, useful for
XX diagnosis, prognosis and treatment of solid tumors, also for drug
XX screening.
XX Claim 8; SEQ ID NO 2; 38pp; French.
XX The present invention relates to monoclonal antibody (Mab) that
XX recognizes specifically the human or murine aurora-A kinase binds to
XX membranes that contain, can detect and optionally purify by
XX immunoprecipitation, stains biological tissues where is secreted and does
XX not inhibit the enzymatic activity of Mab. Cytostatic. Mab are used for
XX in vitro diagnosis and prognosis of cancers in humans and animals,
XX particularly breast, gastric and colorectal cancer; for treatment of
XX these cancers; and to screen for inhibitors of Mab. The present sequence
XX represents the monoclonal antibody of the invention.
XX Sequence 403 AA;
XX
XX Query Match 99.7%; Score 2104; DB 8; Length 403;
XX Best Local Similarity 99.8%; Pred. No. 3.5e-186;
XX Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQPPQNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQPPQNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
QY 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENPPEELASKQKN 120
DB 61 AQLVSSHKPVQKQKQLQATSVPHVSRPLNNTQSKQPLPSAPENPPEELASKQKN 120
QY 121 EESKKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHOLRR 180
DB 121 EESKKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHOLRR 180
QY 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVTVRELOKLSKDFEORTATYTTEL 240
DB 181 EVEIQSHLRHPNLRILYGFHDATRVYLILEYAPLGTVTVRELOKLSKDFEORTATYTTEL 240
QY 241 ANALSYCHSKRVTHRIDIKPENLLGSAGELKIAFDGWSVHAPSSRRITLCGLDYLPPPM 300

Db 241 ANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCEFLVGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGLVCEFLVGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLI 360
QY 361 SRLKHNPSQRMPLREVLEHPHWITANSSKPNCKNESASKOS 403
Db 361 SRLKHNPSQRMPLREVLEHPHWITANSSKPNCKNESASKOS 403
RESULT 14
ADK67720
ID ADK67720 standard; protein; 403 AA.
XX
AC ADK67720;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Human modifier of AXIN (MAX) polypeptide.
XX
XX Human; modifier of AXIN; MAX; cytosstatic; gene therapy; protein kinase;
KW enzyme.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 31 /note= "Encoded by TTT"
FT FT
FT Misc-difference 104 /note= "Encoded by TC"
FT FT
FT Misc-difference 128 /note= "Encoded by TG"
FT FT
FT Misc-difference 235 /note= "Encoded by AACT"
FT FT
FT Misc-difference 240 /note= "Encoded by TT"
FT FT
XX
PN WO2004013308-A2.
XX
XX
FD 12-FEB-2004.
XX
XX 06-AUG-2003; 2003WO-US024560.
XX
XX 06-AUG-2002; 2002US-0401534P.
PR 16-SEP-2002; 2002US-0411153P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Gendreau SB, Dora EG, Lickteig K, Amundsen CD;
XX
XX WPI; 2004-157122/15.
DR N-PSDB; ADK67713.
XX
XX Identifying a candidate AXIN pathway-modulating agent, useful in
PT diagnosing and treating cancer, comprises providing an assay system
PT comprising a MAX polypeptide or nucleic acid.
XX
XX Example 1; SEQ ID NO 11; 74pp; English.
XX
XX The present sequence is that of a human modifier of AXIN (MAX)
CC polypeptide characterised as a serine/threonine kinase. Genetic screens
CC were designed to identify modifiers of the axin pathway in Caenorhabditis
CC elegans, where a reduction of function pry-1 (axin) mutant was used.
CC Genes causing altered phenotypes were isolated, and their human
CC homologues, termed MAX, were identified, including the present sequence.
CC These MAX polynucleotides and polypeptides are attractive targets for the
CC treatment of pathologies associated with a defective AXIN signalling
CC pathway, such as cancer. Modulation of MAX or its binding partner is
CC useful for understanding the association of the AXIN pathway and its
CC members in normal and disease conditions and for developing diagnostic
CC and therapeutic modalities for AXIN related pathologies. MAX-modulating
CC agents that act by inhibiting or enhancing MAX expression, directly or

CC indirectly, e.g. by affecting MAX function can be identified using
CC methods of the invention. MAX modulating agents are useful in diagnosis,
CC therapy and pharmaceutical development. Preferred MAX modulating agents
CC include antisense and phosphorothioate morpholino oligomers.
XX
SQ Sequence 403 AA;
Query Match 99.7%; Score 2104; DB 8; Length 403;
Best Local Similarity 99.8%; Pred. NO. 3.5e-186;
Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDRSKENCISGRVVKATAPVGGPKRVLTQOQPCCQNPPLVNSGQARVLCPSNSSORVPIQ 60
Db 1 MDRSKENCISGRVVKATAPVGGPKRVLTQOQPCCQNPPLVNSGQARVLCPSNSSORVPIQ 60
QY 61 AOKLVSSHKPVQONOKOLOQATSVPHVPSRPLNNTQKSKQPLPSAPENNPEELASKQKN 120
Db 61 AOKLVSSHKPVQONOKOLOQATSVPHVPSRPLNNTQKSKQPLPSAPENNPEELASKQKN 120
QY 121 BESKRWALEDFEIGRPLGKGFQNVYLAREKQSKFILALKVLFKAQLEKAGVHQLRR 180
Db 121 BESKRWALEDFEIGRPLGKGFQNVYLAREKQSKFILALKVLFKAQLEKAGVHQLRR 180
QY 181 EVEIOSHLRHPNIRLYGYFHDATRVYLILEYAPIGTVYRELOKLSKDEORTATVITEL 240
Db 181 EVEIOSHLRHPNIRLYGYFHDATRVYLILEYAPIGTVYRELOKLSKDEORTATVITEL 240
QY 241 ANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM 300
Db 241 ANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGLVCEFLVGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLI 360
Db 301 IEGRMHDEKVDLWSLGLVCEFLVGKPPPEANTYQETKYRISRVEFTFPDFVTEGARDLI 360
QY 361 SRLKHNPSQRMPLREVLEHPHWITANSSKPNCKNESASKOS 403
Db 361 SRLKHNPSQRMPLREVLEHPHWITANSSKPNCKNESASKOS 403
RESULT 15
ADW72205
ID ADM72205 standard; protein; 403 AA.
XX
AC ADM72205;
XX
DT 17-JUN-2004 (first entry)
XX
XX Human TASK104 polypeptide.
XX
XX TASK; tumour-associated kinase; cytosstatic; tumour antigen;
KW cell proliferative disorder; cancer; transgenic; human.
XX
XX Homo sapiens.
XX
XX WO2004024064-A2.
XX
PD 25-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027894.
XX
XX 11-SEP-2002; 2002US-0410166P.
PR (GETH) GENENTECH INC.
XX
XX Desauvage FJ, Wood WT, Zhang Z;
XX WPI; 2004-282985/26.
DR N-PSDB; ADM72204.
XX
XX New tumor-associated kinase nucleic acids and polypeptides, useful as
PT hybridization probes for isolating full length TASK DNA, for generating
PT transgenic animals, in chromosome identification, or for tissue typing.

```
XX Claim 12; SEQ ID NO 10; 163pp; English.
XX
XX The invention relates to new isolated tumour-associated kinase (TASK)
CC nucleic acid molecules and encoded polypeptides. Cytostatic. The
CC antibody, oligopeptide or organic molecule that binds to the TASK
CC polypeptide are useful for treating a mammal having a tumour comprising
CC cells expressing the polypeptide. Antagonists of TASK are useful for
CC treating or preventing a cell proliferative disorder (e.g. cancer)
CC associated with increased expression or activity of TASK polypeptide. The
CC TASK polynucleotides and polypeptides may be used as hybridization probes
CC for isolating full length TASK DNA for generating transgenic animals, in
CC chromosome identification, or for tissue typing. The present sequence
XX represents a human TASK polypeptide.
XX
SQ Sequence 403 AA;
    Query Match          99.7%; Score 2104; DB 8; Length 403;
    Best Local Similarity 99.8%; Pred. No. 3.5e-186;
    Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
QY 61 AOKLVSSHKPQVQKQKQLOQATSVPHVSRPLNNTQSKQPLPSAPENNPEELASKQKN 120
DB 61 AOKLVSSHKPQVQKQKQLOQATSVPHVSRPLNNTQSKQPLPSAPENNPEELASKQKN 120
QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLPKAQLEKAGVEHQLRR 180
DB 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLPKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240
DB 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLPKPPPEANTYQETKYRISRVETFPDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYEFVLPKPPPEANTYQETKYRISRVETFPDFVTEGARDLI 360
QY 361 SRLLEKNPSORPMLREVLHPMTITANSSKPSNCKNESASKQS 403
DB 361 SRLLEKNPSORPMLREVLHPMTITANSSKPSNCKNESASKQS 403
RESULT 16
ID ABP97366
XX ABP97366 standard; protein; 403 AA.
AC ABP97366;
XX
XX 10-MAY-2003 (first entry)
DT
DE Human serine/threonine kinase 15 (STK15).
XX
KW Human; serine/threonine kinase 15; STK15; Aurora2; cell cycle;
KW chromosome 20; centrosome-associated kinase; cancer susceptibility;
KW single nucleotide polymorphism; SNP; genetic diagnosis; prognosis;
KW detection; diagnosis; cancer; malignant astrocytoma; glioblastoma;
KW medulloblastoma; gastric cancer; colorectal cancer; colorectal adenoma;
KW acute myelogenous leukaemia; lung cancer; renal cancer; leukaemia;
KW breast cancer; prostate cancer; endometrial cancer; neuroblastoma;
KW enzyme.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 31
FT
```

```
FT FT /label= Phe, Ile
FT FT /note= "Encoded by WTT. This position represents a
FT FT polymorphic site"
FT FT Misc-difference 57
XX XX /note= "Encoded by ATT"
PN WO2003012046-A2.
XX 13-FEB-2003.
XX 29-JUL-2002; 2002WO-US024115.
XX 27-JUL-2001; 2001US-0308911P.
XX 28-NOV-2001; 2001US-0334146P.
XX (REGC ) UNIV CALIFORNIA.
XX Toland AB, Balmain A;
XX WPI; 2003-239517/23.
XX N-PSDB; AB275005.
XX Determining cancer susceptibility in a human subject comprises
XX identifying in a nucleic acid sample from the subject, a nucleotide
XX occurrence of a single polynucleotide polymorphism (SNP) of the STK15
XX gene.
XX Claim 63; Page 85-86; 92pp; English.
XX
XX The invention relates to a method for determining cancer susceptibility
XX in a human patient. The method involves determining the identity of the
XX nucleotide at position 457 of the serine/threonine kinase 15 (STK15) DNA
XX (AB275005). This site is a T/A single nucleotide polymorphism (SNP) in
XX the coding region of the DNA, resulting in either a Phe or Ile residue at
XX position 31 in the corresponding STK15 protein (ABP97366). The A457
XX (Ile31) allele (see AB275006, ABP97367) is associated with an increased
XX cancer susceptibility. STK15 (also known as STK6 and Aurora2) is a
XX centrosome-associated kinase that is highly expressed at the G2 and M
XX phase of the cell cycle, and its gene is located on chromosome 20. The
XX method of the invention are useful for determining cancer susceptibility
XX and for prognosing, detecting and/or diagnosing cancers such as malignant
XX astrocytoma, glioblastoma, medulloblastoma, gastric cancer, colorectal
XX cancer, colorectal adenoma, acute myelogenous leukemia, lung cancer,
XX renal cancer, leukaemia, breast cancer, prostate cancer, endometrial
XX cancer and neuroblastoma. This sequence represents human STK15
XX
SQ Sequence 403 AA;
    Query Match          99.7%; Score 2103; DB 6; Length 403;
    Best Local Similarity 99.8%; Pred. No. 4.3e-186;
    Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60
QY 61 AOKLVSSHKPQVQKQKQLOQATSVPHVSRPLNNTQSKQPLPSAPENNPEELASKQKN 120
DB 61 AOKLVSSHKPQVQKQKQLOQATSVPHVSRPLNNTQSKQPLPSAPENNPEELASKQKN 120
QY 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLPKAQLEKAGVEHQLRR 180
DB 121 EESKKQWALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLPKAQLEKAGVEHQLRR 180
QY 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240
DB 181 EVEIQSHLRHPNLRILYGYFHDATRVYLILEYAPLGTVTVRELQKSKFDEQRTATITEL 240
QY 241 ANALSYCHSKRVTHRDIKPENLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
DB 241 ANALSYCHSKRVTHRDIKPENLLSAGELKIADFGWSVHAPSSRRRTTLCGTLDYLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYEFVLPKPPPEANTYQETKYRISRVETFPDFVTEGARDLI 360
```


Db 301 IEGRMHDEKVDLWSLGVLCYFELVGVKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
361 SRLLNKPNPSQRPMLREVLEHPHWITANSSKPSNCKESASKOS 403
361 SRLLNKPNPSQRPMLREVLEHPHWITANSSKPSNCKESASKOS 403
RESULT 17
ADJ31727
ID ADJ31727 standard; protein; 403 AA.
AC ADJ31727;
DT 22-APR-2004 (first entry)
XX Human mitotic kinase hARK.
XX Human; enzyme; SAK; Snk Akin Kinase; serine/threonine protein kinase;
KW mitotic kinase; cellular proliferation; chemosensitivity; cancer;
KW proliferative disorder; cytostatic; hARK.
XX Homo sapiens.
XX US2003027756-A1.
XX 06-FEB-2003.
XX 21-DEC-2001; 2001US-00026021.
XX 01-AUG-2001; 2001US-0309632P.
XX (RIGE-) RIGEL PHARM INC.
XX Hitoshi Y, Demo S, Jenkins Y;
XX WPI; 2003-479546/45.
XX Modulating cellular proliferation in subject, by administering
PT serine/threonine protein kinase involved in modulation of cellular
PT proliferation and cell cycle regulation, or a nucleic acid encoding the
PT polypeptide.
XX Example 1; Fig 2; 41pp; English.
XX The invention relates to modulating (M1) cellular proliferation in a
CC subject, involves administering to the subject a serine/threonine protein
CC kinase involved in modulation of cellular proliferation and cell cycle
CC regulation (SAK polypeptide, Snk Akin Kinase, a mitotic kinase) encoded
CC by a nucleic acid that hybridises under stringent conditions to a nucleic
CC acid encoding a polypeptide appearing as ADJ31723. Also included are
CC identifying (M2) a compound capable of interfering with binding of SAK or
CC its fragment (by combining SAK or its fragment with Chk2 polypeptide and
CC the compound, where SAK or its fragment has kinase activity, and
CC determining the binding of SAK or its fragment to Chk2), identifying (M3)
CC a compound that modulates cellular proliferation (by contacting the
CC compound with SAK, and determining the functional effect of the compound
CC on SAK), identifying (M4) a compound that modulates cellular
CC proliferation or chemosensitivity, (by contacting the compound with SAK
CC or its fragment, and determining the physical effect of the compound on
CC SAK), determining the chemical or phenotypic effect of the compound upon
CC a cell comprising SAK or its fragment and modulating (M5) cellular
CC proliferation in a subject (by administering to the subject a compound
CC identified by M3). M1 or M5 is useful for modulating cellular
CC proliferation in a subject, preferably a human having cancer. M2 is
CC useful for identifying a compound capable of interfering with binding of
CC SAK or its fragment. M3 is useful for identifying a compound that
CC modulates cellular proliferation. M4 is useful for identifying a compound
CC that modulates cellular proliferation or chemosensitivity, where the
CC compound is an antibody, antisense molecule, small organic molecule, or
CC circular peptide. M1 or M5 or the compound identified by M3 or M4 is
CC useful for treating cancer and other proliferative disorders. The present
CC sequence represents a human mitotic kinase similar to SAK.

XX SQ Sequence 403 AA;
Query Match 99.3%; Score 2095; DB 7; Length 403;
Best Local Similarity 99.3%; Pred. No. 2.4e-185;
Matches 400; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDRSKENCISGFPVKATAPVGGPKRVLVVQQFPQNPPLVNSGQAOQVLCPSNSSQRPVLO 60
DB 1 MDRSKENCISGFPVKATAPVGGPKRVLVVQQFPQNPPLVNSGQAOQVLCPSNSSQRPVLO 60
QY 61 AOKLVSSHHPVONQKQKQLOQATSVPHPVSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 120
DB 61 AOKLVSSHHPVONQKQKQLOQATSVPHPVSRPLNNTOKSKOPLPSAPENNPPEELASKQKN 120
QY 121 BESKKROWALEDFEIGRPLGKGFNGVYLAREKQSKFILALKVLFKAQLEKAGVEHOLRR 180
DB 121 BESKKROWALEDFEIGRPLGKGFNGVYLAREKQSKGILALKVLFKAQLEKAGVEHOLRR 180
QY 181 EYEIQSHLHPNLRILYGVFHDATRVYLILEYAPLGTVYVRELQKLSKFDEQRTATVITEL 240
DB 181 EYEIQSHLHPNLRILYGVFHDATRVYLILEYAPLGTVYVRELQKLSKFDEQRTATVITEL 240
QY 241 ANALSYCHSKRVIHRDIKPNENLLGSAGELKTADFGWSVHAPSSRRITLCGTLDVLPPEM 300
DB 241 ANALSYCHSKRVIHRDIKPNENLLGSAGELKTADFGWSVHAPSSRRITLCGTLDVLPPEM 300
QY 301 IEGRMHDEKVDLWSLGVLCYFELVGVKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
DB 301 IEGRMHDEKVDLWSLGVLCYFELVGVKPPPEANTYQETVKRISRVETFPDFVTEGARDLI 360
QY 361 SRLLNKPNPSQRPMLREVLEHPHWITANSSKPSNCKESASKOS 403
DB 361 SRLLNKPNPSQRPMLREVLEHPHWITANSSKPSNCKESASKOS 403
RESULT 18
ABR61579
ID ABR61579 standard; protein; 402 AA.
XX ABR61579;
XX 15-JAN-2004 (first entry)
XX Human HsAIRK-1 (Aurora B) protein.
XX DE RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; HsAIRK-1;
XX KW Aurora B.
XX OS Homo sapiens.
XX PN WO2003087395-A2.
XX PD 23-OCT-2003.
XX 15-APR-2003; 2003WO-IB002972.
XX 15-APR-2002; 2002US-0372483P.
XX (INRM) INERM INST NAT SANTE & RECH MEDICALE.
XX Garbay C, Gigoux V, Canonis J, L'hoste S, Samson J;
XX WPI; 2003-845340/78.
XX N-PSDB; ACF58068.
XX Identifying anti-tumoral compounds, comprises determining the capacity of
PT a compound to inhibit interaction between RasGAP and Drosophila
PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
PT aurora binding protein.
XX Disclosure; Page 59-60; Opp; English.
XX PS

CC The invention relates to identifying a biologically active compound with
 CC anti-tumoural properties, where the compound is studied for its capacity
 CC to inhibit the interaction between: (a) RasGAP and the Drosophila
 CC melanogaster Aurora kinase or an orthologue of the kinase, or its
 CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
 CC protein and the D. melanogaster Aurora kinase or an orthologue of the
 CC kinase, or its fragment. The method is useful for identifying anti-
 CC tumoural agents. The present sequence represents a human HAIRK-1 (Aurora
 CC B) protein, an orthologue of the D. melanogaster Aurora kinase
 XX
 XX
 SQ Sequence 402 AA;

Query Match 91.7%; Score 1935.5; DB 7; Length 402;
 Best Local Similarity 92.9%; Pred. No. 1.5e-170;
 Matches 378; Conservative 3; Mismatches 17; Indels 9; Gaps 3;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSQRVPLQ 60
 DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSQRVPLQ 60
 QY 61 AQLVSSHKPVQKQKQLQATSPVHPVSRPLNNTOKSKQPLPS----APENNPEELAS 116
 DB 61 AQLVSSHKPVQKQKQLQATSPVHPVSRPLNNTOKSKQPLPSHLKILRRWHQN--R 118
 QY 117 KQNEESKRWQMALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEH 176
 DB 119 KMKNQ---KEAVALDEFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEH 175
 QY 177 QLRREVEIQSHLRHPNRLRYGYFHDATRVYLILEYAPLGTGVYRELQKSKFDEORTATY 236
 DB 176 QLRREVEIQSHLRHPNRLRYGYFHDATRVYLILEYAPLGTGVYRELQKSKFDEORTANL 235
 QY 237 ITLANALSYCHSKRVIHRDIPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLIDYL 296
 DB 236 YNRIANALSYCHSKRVIHRDIPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLIDYL 295
 QY 297 PPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKISRVEFTFPDFVTEGA 356
 DB 296 PPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKISRVEFTFPDFVTEGA 355
 QY 357 RDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKESASKOS 403
 DB 356 RDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKESASKOS 402

RESULT 19
 ADD89969
 ID ADD89969 standard; protein; 402 AA.
 XX
 AC ADD89969;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 XX Human cancer-associated protein kinase STK6.
 DE
 XX STK6; protein kinase; enzyme; cancer; cytostatic; immunosuppressive;
 KW antidiabetic; antirheumatic; antiarthritic; antipsoriatic;
 KW antiangiogenic; antiarteriosclerotic; antiinflammatory; vulnery;
 KW gynaecological; neuroprotective; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003083096-A2.
 XX
 PD 09-OCT-2003.
 XX
 PF 21-MAR-2003; 2003WO-CA000409.
 XX
 PR 28-MAR-2002; 2002US-0368853P.
 XX
 PA (KINE-) KINETEK PHARM INC.
 XX
 PI Delaney AD;

XX WPI; 2003-833542/77.
 DR N-PSDB; ADD89968.
 XX
 PT New nucleic acids encoding cancer associated protein kinases, useful as
 PT targets for screening pharmaceutical agents that inhibit the growth of
 PT tumor cells, or for diagnosing and treating cancer, inflammation or
 PT autoimmune disease.
 XX
 XX Claim 1; Page 73-74; 91pp; English.

CC The present sequence is the protein sequence of the human cancer-
 CC associated protein kinase, STK6. Serine/threonine kinase 6 (STK6),
 CC otherwise known as Aik, is an aurora/IPLI-like kinase possibly involved
 CC in centrosome function. STK6 gene expression is significantly up-
 CC regulated in cancers of the liver, muscle, placenta, and prostate. STK6
 CC is one of a set of protein kinases that are shown by the invention to be
 CC over-expressed in hyper-proliferative cells. These protein kinases
 CC provide targets for drug screening for agents effective in inhibiting the
 CC growth or metastasis of tumour cells, and for determining other molecular
 CC targets in kinase signal transduction pathways involved in transformation
 CC and growth of tumour cells. A claimed method for inhibiting the growth of
 CC a cancer cell involves down-regulating the activity of the protein kinase
 CC using an antisense sequence or inhibitor of kinase activity, especially
 CC where the cancer cell is a breast, liver, colon, muscle, prostate,
 CC kidney, lung, placental or uterine cancer cell. Detection of over-
 CC expression in cancers provides a useful diagnostic for predicting patient
 CC prognosis and probability of drug effectiveness. Agents that specifically
 CC bind the protein kinases can be used for treatment and visualisation of
 CC tumours in patients. The protein kinase polypeptides and nucleic acids
 CC may also be used for treating hyperproliferative diseases, such as
 CC autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid
 CC arthritis, psoriasis, atherosclerosis, inflammation, scarring,
 CC endometriosis and angiogenesis.
 XX
 XX Sequence 402 AA;

Query Match 91.7%; Score 1935.5; DB 7; Length 402;
 Best Local Similarity 92.9%; Pred. No. 1.5e-170;
 Matches 378; Conservative 3; Mismatches 17; Indels 9; Gaps 3;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSQRVPLQ 60
 DB 1 MDRSKENCISGPVKATAPVGGPKRVLVTQFPQCNPLPVNSGQQRVLCPSNSQRVPLQ 60
 QY 61 AQLVSSHKPVQKQKQLQATSPVHPVSRPLNNTOKSKQPLPS----APENNPEELAS 116
 DB 61 AQLVSSHKPVQKQKQLQATSPVHPVSRPLNNTOKSKQPLPSHLKILRRWHQN--R 118
 QY 117 KQNEESKRWQMALEDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEH 176
 DB 119 KMKNQ---KEAVALDEFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEH 175
 QY 177 QLRREVEIQSHLRHPNRLRYGYFHDATRVYLILEYAPLGTGVYRELQKSKFDEORTATY 236
 DB 176 QLRREVEIQSHLRHPNRLRYGYFHDATRVYLILEYAPLGTGVYRELQKSKFDEORTANL 235
 QY 237 ITLANALSYCHSKRVIHRDIPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLIDYL 296
 DB 236 YNRIANALSYCHSKRVIHRDIPENLLGSAGELKIADFGWSVHAPSSRRRTTLCGTLIDYL 295
 QY 297 PPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKISRVEFTFPDFVTEGA 356
 DB 296 PPEMIEGRMHDEKVDLWSLGVLCYEFVLGKPPPEANTYQETKYKISRVEFTFPDFVTEGA 355
 QY 357 RDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKESASKOS 403
 DB 356 RDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKESASKOS 402

RESULT 20
 AAO18740
 ID AAO18740 standard; protein; 403 AA.


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XX PR 10-OCT-2001; 2001GB-00024299.
XX PA (ASTR ) ASTRAZENECA AB.
XX PA (ASTR ) ASTRAZENECA UK LTD.
XX PI Anderson M, Keen NJ, Pannifer ADB, Paupit RA, Rowsell S;
XX DR WPI; 2003-403104/38.
XX
XX Novel crystalline form of polypeptide comprising catalytic domain of
PT Aurora kinase, whose atomic coordinate data is useful for designing or
PT selecting Aurora chemical inhibitor, and for designing an Aurora protein.
XX
XX Example 1; Page 117; 137pp; English.
XX
XX The invention relates to the three-dimensional structure of human Aurora
CC A kinase. The invention describes the methods used to prepare and
CC crystallise truncated mutant forms of human Aurora A kinase comprising
CC the catalytic domain, which were then subjected to X-ray crystallography
CC to generate atomic coordinates. The mutant forms of Aurora A used in the
CC invention all contain a T287D substitution, which produces a mimic of the
CC activated protein which can be provided as a homogeneous sample (native
CC Aurora A kinase is activated by phosphorylation of T287). Two crystalline
CC forms of the Aurora A kinase catalytic domain were produced - one
CC complexed with the hydrolysable ATP analogue ANP-FNP, and one complexed
CC with a synthetic inhibitor. The ATP analogue was found to occupy a cleft
CC between the N-terminal domain (residues 125-208) and the C-terminal
CC domain (residues 215-374). Aurora A kinase is a serine/threonine kinase
CC which is involved in cell cycle regulation, with its expression and
CC activity peaking at the G2/M boundary. It has been implicated in
CC oncogenesis - the Aurora A gene maps to chromosome 20q13, a region which
CC is frequently amplified in human tumours including breast and colon
CC tumours, and it is overexpressed in over 50% of primary colorectal
CC tumours. The crystal structure of human Aurora A kinase may be used to
CC select or design chemical modulators of Aurora A kinase, particularly
CC Aurora kinase inhibitors. These modulators may be used to prevent or
CC treat undesirable physical and pharmacological consequences of
CC inappropriate Aurora activity, especially cancers or other
CC hyperproliferative disorders. The Aurora A kinase 3D structure may also
CC be used in designing an Aurora protein or Aurora homologue, and in
CC elucidating the 3D structure of other proteins with structural similarity
CC to Aurora kinases. The present sequence represents a truncated T287D
CC mutant Aurora A kinase sequence which was prepared and crystallised in an
CC example from the invention. This sequence comprises the Aurora A kinase
CC domain and also contains a vector-encoded sequence at the N-terminus
XX
XX Sequence 319 AA;
XX
Query Match 76.5%; Score 1614; DB 6; Length 319;
Best Local Similarity 99.4%; Pred. No. 7.4e-141;
Matches 308; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 94 NTOKSKOPLPSAPENNPPEELASKQNEESKQWALEDFEIGRPLGKGFNGVYLAREK 153
DB :
DB 10 STOKSKOPLPSAPENNPPEELASKQNEESKQWALEDFEIGRPLGKGFNGVYLAREK 69
QY 154 QSKFLLALKVLPKQAEKAGVEHQLRREVEIQSHLRHNPILRLYGFYFHDATRVYLILEVA 213
DB :
DB 70 QSKFLLALKVLPKQAEKAGVEHQLRREVEIQSHLRHNPILRLYGFYFHDATRVYLILEVA 129
QY 214 PLGTVYRELQKLSKPFQRTATYITELANALYSCHSKRVTHRDIKPENLLLSAGELKIA 273
DB :
DB 130 PLGTVYRELQKLSKPFQRTATYITELANALYSCHSKRVTHRDIKPENLLLSAGELKIA 189
QY 274 DFCWSVHAPSSRRRTTCGLTDYLLPPEMIEGRMHDEKVDLWSLGVLCYFELVGKPPPEANT 333
DB :
DB 190 DFCWSVHAPSSRRRTTCGLTDYLLPPEMIEGRMHDEKVDLWSLGVLCYFELVGKPPPEANT 249
QY 334 YQTYTKRISRVETFFDFVTEGARDLISRLKHNPSQRPMLREVLSHPWITANSSKPSNC 393
DB :
DB 250 YQTYTKRISRVETFFDFVTEGARDLISRLKHNPSQRPMLREVLSHPWITANSSKPSNC 309
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QY 394 QNKESASKOS 403
DB :
DB 310 QNKESASKOS 319
XX
XX RESULT 22
XX ABP97472
XX ID ABP97472 standard; protein; 309 AA.
XX AC ABP97472;
XX XX
XX DT 19-SEP-2003 (first entry)
XX XX
XX DE Truncated mutant human Aurora A kinase, [T287] Aurora A (113-400) .
XX
XX KW Aurora A kinase; human; catalytic domain; chromosome 20q13; 3D structure;
XX X-ray crystallography; protein co-ordinate data; serine/threonine kinase;
XX cell cycle regulation; G2/M boundary; oncogenesis;
XX hyperproliferative disorder; cancer; tumour; breast; colon; colorectal;
XX Aurora homologue design; rational drug design; drug screening; enzyme;
XX mutant; mutain.
XX
XX OS Homo sapiens.
XX
XX XX Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT 1. .21
XX FT /note= "pET28a vector-encoded sequence, comprising a
XX FT hexahistidine sequence"
XX FT 33. .117
XX FT /label= N-terminal_domain
XX FT /note= "Corresponds to residues 125-208 of the native
XX FT human Aurora A kinase"
XX FT 118. .123
XX FT /label= ATP binding_pocket
XX FT /note= "Corresponds to residues 209-214 of the native
XX FT human Aurora A kinase. Also referred to as a hinge region
XX FT between the N- and C-terminal domains"
XX FT 119
XX FT Binding-site
XX
XX FT /note= "The peptide carbonyl group of this residue binds
XX FT adenine nitrogen atom N6. Corresponds to residue 210 of
XX FT the native human Aurora A kinase"
XX FT 121
XX FT Binding-site
XX
XX FT /note= "The main chain nitrogen of this residue binds
XX FT adenine nitrogen atom N1. Corresponds to residue 212 of
XX FT the native human Aurora A kinase"
XX FT 124. .283
XX FT Domain
XX FT /label= C-terminal_domain
XX FT /note= "Corresponds to residues 215-374 of the native
XX FT human Aurora A kinase"
XX FT Misc-difference 196
XX FT /note= "Asp replaces wild-type Thr. Corresponds to
XX FT position 287 of the native human Aurora A kinase"
XX
XX WO2003031606-A2.
XX
XX 17-APR-2003.
XX
XX 08-OCT-2002; 2002WO-GB004589.
XX
XX 10-OCT-2001; 2001GB-00024299.
XX
XX (ASTR ) ASTRAZENECA AB.
XX (ASTR ) ASTRAZENECA UK LTD.
XX
XX Anderson M, Keen NJ, Pannifer ADB, Paupit RA, Rowsell S;
XX WPI; 2003-403104/38.
XX
XX Novel crystalline form of polypeptide comprising catalytic domain of
PT Aurora kinase, whose atomic coordinate data is useful for designing or
PT selecting Aurora chemical inhibitor, and for designing an Aurora protein.
XX
```

PS Example 1; Page 119; 137pp; English.

XX The invention relates to the three-dimensional structure of human Aurora

CC A kinase. The invention describes the methods used to prepare and

CC crystallise truncated mutant forms of human Aurora A kinase comprising

CC the catalytic domain, which were then subjected to X-ray crystallography

CC to generate atomic coordinates. The mutant forms of Aurora A used in the

CC invention all contain a T287D substitution, which produces a mimic of the

CC activated protein which can be provided as a homogeneous sample (native

CC Aurora A kinase is activated by phosphorylation of T287). Two crystalline

CC forms of the Aurora A kinase catalytic domain were produced - one

CC complexed with the hydrolysable ATP analogue ANP-PNP, and one complexed

CC with a synthetic inhibitor. The ATP analogue was found to occupy a cleft

CC between the N-terminal domain (residues 125-208) and the C-terminal

CC domain (residues 215-374). Aurora A kinase is a serine/threonine kinase

CC which is involved in cell cycle regulation, with its expression and

CC activity peaking at the G2/M boundary. It has been implicated in

CC oncogenesis - the Aurora A gene maps to chromosome 20q13, a region which

CC is frequently amplified in human tumours including breast and colon

CC tumours, and it is overexpressed in over 50% of primary colorectal

CC tumours. The crystal structure of human Aurora A kinase may be used to

CC select or design chemical modulators of Aurora A kinase, particularly

CC Aurora kinase inhibitors. These modulators may be used to prevent or

CC treat undesirable physical and pharmacological consequences of

CC inappropriate Aurora activity, especially cancers or other

CC hyperproliferative disorders. The Aurora A kinase 3D structure may also

CC be used in designing an Aurora protein or Aurora homologue, and in

CC elucidating the 3D structure of other proteins with structural similarity

CC to Aurora kinases. The present sequence represents a truncated T287D

CC mutant Aurora A kinase sequence which was prepared and crystallised in an

CC example from the invention. This sequence comprises the Aurora A kinase

CC domain and also contains a vector-encoded sequence at the N-terminus

XX Sequence 309 AA;

SQ

Query Match 71.2%; Score 1503; DB 6; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.4e-130;

Matches 287; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 114 LASKQNEESKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLPAQLEKAG 173

DB 22 LASKQNEESKQWALEDEIGRPLGKGFNGVYLAREKQSFILALKVLPAQLEKAG 81

QY 174 VEHLRREVEIQSHLRHNPILRLYGFDATRVYLILEVAPLGTVYRELQKLSKDFEQT 233

DB 82 VEHLRREVEIQSHLRHNPILRLYGFDATRVYLILEVAPLGTVYRELQKLSKDFEQT 141

QY 234 ATYITELANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTLCGTL 293

DB 142 ATYITELANALSYCHSKRVTHRDIKPENLLLSAGELKIADFGWSVHAPSSRRRTLCGTL 201

QY 294 DYLPPEMIEGRMDEKVDLWSGLVCYEFVLGKPPPEANTYQETKYRISRVETFPDFVT 353

DB 202 DYLPPEMIEGRMDEKVDLWSGLVCYEFVLGKPPPEANTYQETKYRISRVETFPDFVT 261

QY 354 EGARDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKNESASK 401

DB 262 EGARDLISRLKHNPSQRPMLREVLEHPWITANSKPSNCKNESASK 309

RESULT 23

ABP97473

ID ABP97473 standard; protein; 300 AA.

XX ABP97473;

AC ABP97473;

XX

XX 19-SEP-2003 (first entry)

DT Truncated mutant human Aurora A kinase, [T287] Aurora A (122-400).

DE

XX Aurora A kinase; human; catalytic domain; chromosome 20q13; 3D structure;

KW X-ray crystallography; protein co-ordinate data; serine/threonine kinase;

KW cell cycle regulation; G2/M boundary; oncogenesis;

KW hyperproliferative disorder; cancer; tumour; breast; colon; colorectal;

KW Aurora homologue design; rational drug design; drug screening; enzyme;

XX mutant; mutuin.

OS Homo sapiens.

OS Synthetic.

XX

PH Key

FT Location/Qualifiers

FT 1..21

FT /note= "pET28a vector-encoded sequence, comprising a

FT hexahistidine sequence"

FT 24..108

FT /label= N-terminal domain

FT /note= "Corresponds to residues 125-208 of the native

FT human Aurora A kinase"

FT 109..114

FT /label= ATP_binding_pocket

FT /note= "Corresponds to residues 209-214 of the native

FT human Aurora A kinase. Also referred to as a hinge region

FT between the N- and C-terminal domains"

FT 110

FT /note= "The peptide carbonyl group of this residue binds

FT adenine nitrogen atom N6. Corresponds to residue 210 of

FT the native human Aurora A kinase"

FT 112

FT /note= "The main chain nitrogen of this residue binds

FT adenine nitrogen atom N1. Corresponds to residue 212 of

FT the native human Aurora A kinase"

FT 115..124

FT /label= C-terminal_domain

FT /note= "Corresponds to residues 215-374 of the native

FT human Aurora A kinase"

FT Misc-difference 187

FT /note= "Asp replaces wild-type Thr. Corresponds to

FT position 287 of the native human Aurora A kinase"

XX WO2003031606-A2.

PN 17-APR-2003.

XX

PD 08-OCT-2002; 2002WO-GB004589.

PF 10-OCT-2001; 2001GB-00024299.

XX (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.

XX

PI Anderson M, Keen NJ, Pannifer ADB, Pauptit RA, Rowsell S;

XX WPI; 2003-403104/38.

DR

XX

XX Novel crystalline form of polypeptide comprising catalytic domain of

PT Aurora kinase, whose atomic coordinate data is useful for designing or

PT selecting Aurora chemical inhibitor, and for designing an Aurora protein.

XX

PS Example 1; Page 119; 137pp; English.

XX

XX The invention relates to the three-dimensional structure of human Aurora

CC A kinase. The invention describes the methods used to prepare and

CC crystallise truncated mutant forms of human Aurora A kinase comprising

CC the catalytic domain, which were then subjected to X-ray crystallography

CC to generate atomic coordinates. The mutant forms of Aurora A used in the

CC invention all contain a T287D substitution, which produces a mimic of the

CC activated protein which can be provided as a homogeneous sample (native

CC Aurora A kinase is activated by phosphorylation of T287). Two crystalline

CC forms of the Aurora A kinase catalytic domain were produced - one

CC complexed with the hydrolysable ATP analogue ANP-PNP, and one complexed

CC with a synthetic inhibitor. The ATP analogue was found to occupy a cleft

CC between the N-terminal domain (residues 125-208) and the C-terminal

CC domain (residues 215-374). Aurora A kinase is a serine/threonine kinase

CC which is involved in cell cycle regulation, with its expression and

CC activity peaking at the G2/M boundary. It has been implicated in

CC oncogenesis - the Aurora A gene maps to chromosome 20q13, a region which

is frequently amplified in human tumours including breast and colon tumours, and it is overexpressed in over 50% of primary colorectal tumours. The crystal structure of human Aurora A kinase may be used to select or design chemical modulators of Aurora kinase, particularly Aurora kinase inhibitors. These modulators may be used to prevent or treat undesirable physical and pharmacological consequences of inappropriate Aurora activity, especially cancers or other hyperproliferative disorders. The Aurora A kinase 3D structure may also be used in designing an Aurora protein or Aurora homologue, and in elucidating the 3D structure of other proteins with structural similarity to Aurora kinases. The present sequence represents a truncated T287D mutant Aurora A kinase sequence which was prepared and crystallised in an example from the invention. This sequence comprises the Aurora A kinase domain and also contains a vector-encoded sequence at the N-terminus

XX Sequence 300 AA;

Query Match 69.2%; Score 1460; DB 6; Length 300;
Best Local Similarity 99.6%; Pred. No. 1.3e-126;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 123 SKKQWALEDFEIGRPLGKGFVNLAREKQSKFLLALKVLFKAQLEKAGVEHQLRREV 182
DB 22 SKKQWALEDFEIGRPLGKGFVNLAREKQSKFLLALKVLFKAQLEKAGVEHQLRREV 81
QY 183 EIQSHLRHPNLRILYGFHDATRVYLILEVAPLGTGVYRELQKLSKDFEQRATYITELAN 242
DB 82 EIQSHLRHPNLRILYGFHDATRVYLILEVAPLGTGVYRELQKLSKDFEQRATYITELAN 141
QY 243 ALSVCHSKRVIHRDIPENLLIGSAGELKTADFGWSVHAPSSRRRTLCGLDYLPPEMIE 302
DB 142 ALSVCHSKRVIHRDIPENLLIGSAGELKTADFGWSVHAPSSRRRTLCGLDYLPPEMIE 201
QY 303 GRMHDEKVDLWSGLVCYELVGLKPFPEANTYQETVKRISRVFTFPDFVTEGARDLISR 362
DB 202 GRMHDEKVDLWSGLVCYELVGLKPFPEANTYQETVKRISRVFTFPDFVTEGARDLISR 261
QY 363 LKHNPSQRPMLREVLEHPWITANSKPSNCQKESASK 401
DB 262 LKHNPSQRPMLREVLEHPWITANSKPSNCQKESASK 300

RESULT 24

ADK71858
ID ADK71858 standard; protein; 248 AA.

XX ADK71858;

XX 20-MAY-2004 (first entry)

DE Human kinase and phosphatase KPP-35 protein.

XX human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotrophic; antiinflammatory; antianginal; anti-HIV;
KW anti-allergic; antiasthmatic; immunosuppressive; anti-thyroid;
KW dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; uterogonic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipemic; antiparasitic;
KW antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme.

OS Homo sapiens.

XX WO2004018641-A2.

XX 04-MAR-2004.

XX 25-AUG-2003; 2003WO-US026635.

XX 26-AUG-2002; 2002US-0406172P.

PR

PR 25-SEP-2002; 2002US-0413910P.
PR 27-SEP-2002; 2002US-0414296P.
PR 11-OCT-2002; 2002US-0417821P.

XX (INCY-) INCYTE CORP.

XX Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BW, Jin P, Wilson AD, Yue H, Gietzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;

XX WPI: 2004-226830/21.

DR N-PSDB; ADK71917.

XX New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.

XX Claim 1; SEQ ID NO 35; 347pp; English.

XX The invention relates to a novel isolated polypeptide which is a human
CC kinase and phosphatase (kpp). The polypeptide of the invention
CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
CC vasotrophic, antiinflammatory, antianginal, anti-HIV, antiallergic,
CC antiasthmatic, immunosuppressive, antithyroid, dermatological,
CC antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective,
CC osteopathic, antirheumatic, uterogonic, ophthalmological, antirheumatic,
CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic,
CC haemostatic, cytostatic, antilipemic, antiparasitic, antihelminthic,
CC antibacterial, virucide, protozoacide and fungicide activities. The
CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
CC antagonists may be useful for diagnosing, treating or preventing
CC disorders such as cardiovascular diseases, immune system disorders,
CC neurological disorders, disorders affecting growth and development, cell
CC proliferative disorders and viral, bacterial, fungal, parasitic,
CC protozoan or helminthic infections. Furthermore, the molecules of the
CC invention may be useful for creating transgenic animals to model human
CC disease and during gene therapy. The current sequence is that of a human
CC KPP protein of the invention.

XX Sequence 248 AA;

Query Match 57.6%; Score 1215; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5.6e-104;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60

DB 1 MDRSKENCISGPVKATAPVGGPKRVLTQOFPQCNPLPVNSGOAQRVLCPSNSSQRVPLQ 60

QY 61 AOKLVSSHKPVQNOKQLOQATSVHPVSRPLNNTOKSKOPLPSAPENNPEELASKOKN 120

DB 61 AOKLVSSHKPVQNOKQLOQATSVHPVSRPLNNTOKSKOPLPSAPENNPEELASKOKN 120

QY 121 EESKKQWALEDFEIGRPLGKGFVNLAREKQSKFLLALKVLFKAQLEKAGVEHQLR 180

DB 121 EESKKQWALEDFEIGRPLGKGFVNLAREKQSKFLLALKVLFKAQLEKAGVEHQLR 180

QY 181 EYEIQLRHPNLRILYGFHDATRVYLILEVAPLGTGVYRELQKLSKDFEQRAT 235

DB 181 EYEIQLRHPNLRILYGFHDATRVYLILEVAPLGTGVYRELQKLSKDFEQRAT 235

RESULT 25

AAW18083

ID AAW18083 standard; protein; 344 AA.

XX AAW18083;

XX 07-SEP-1997 (first entry)

XX DT

DE Human Aurora-1.
 XX Aurora-1; signal transduction; protein kinase; tumour; cancer;
 KW protein kinase; gene therapy; diagnosis; antibody.
 XX Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 1..74
 FT Domain /label= N-terminal_domain
 FT Domain 74..344
 FT Modified-site /label= Kinase_domain
 FT /label= Phosphorylation
 FT /note= "cAMP-dependent protein kinase phosphorylation
 FT site conserved in AUR-2 and yeast and Drosophila
 FT homologues"
 FT Misc-difference 265
 FT /note= "deduced residue from some cDNA clones is Gly"
 PN - WO9722702-A1.
 XX 26-JUN-1997.
 XX 25-NOV-1996; 96WO-US018859.
 PR 18-DEC-1995; 95US-0008809P.
 PR 14-AUG-1996; 96US-0023943P.
 XX (SUGB-) SUGEN INC.
 XX Plowman GD, Mossie KG;
 DR WPI; 1997-341693/31.
 DR N-PSDB; AAT67289.
 XX Aurora-1 and Aurora-2 and related genes - useful in tumour gene therapy.
 PS Claim 3; Page 82-83; 98pp; English.
 CC Novel human proteins, termed Aurora-1 (AAW18083) and Aurora-2 (AAW18084)
 CC (AUR-1 and AUR-2), are related serine/threonine kinases with short N-
 CC terminal extensions that appear to be involved in cancer and/or signal
 CC transduction disorders. Their amino acid sequences were deduced from
 CC pancreatic tumour cDNA clones (AAT67289-90). AUR-1 and AUR-2 appear to
 CC regulate nuclear division, with disruption of their signaling resulting
 CC in polyploid cells. AUR-1 RNA is broadly expressed in rapidly dividing
 CC cells from normal and tumour tissues. AUR polypeptides can be expressed
 CC in host cells and used to raise diagnostic antibodies and to screen for
 CC compounds that interact with AUR-1 and/or AUR-2
 XX Sequence 344 AA;
 SQ
 Query Match 50.1%; Score 1057.5; DB 2; Length 344;
 Best Local Similarity 63.2%; Pred. No. 3.7e-89;
 Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
 QY 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKQKNVESKK-----RQWA 129
 DB 22 STLPRQVLR-----KEPVTFSALVLMRSRNVQPTAAPGQKWMENSGTDPDLTRHFT 73
 QY 130 LEDFEGRLPGKGFNGVYLAREKQSKFILALKVLFKAOLEKAGVHQHRLRREVEIQSHLR 189
 DB 74 IDDFEIGRLPGKGFNGVYLAREKSHFIVALKVLFKSIQIEKGEVHQHRLREIEIOAHLH 133
 QY 190 HPNILRYGYFHDATRYVILEYAPGTGVYRELQKLSKFEQRTATYITELANALSYCHS 249
 DB 134 HPNILRLYNYFYDRRIYVILEYAPRGELYKELOKSCTFEQRTATIMEELADALMYCHG 193
 QY 250 KRVIHEDIKPNLLGSAGELKTDGWSVHAPSSRTTLTGTLVDYLPPEMIEGRMHDEK 309
 DB 194 KRVIHEDIKPNLLGLGKELKTDGWSVHAPSLRRKTCGTLVDYLPPEMIEGRMHNEK 253

QY 310 VDLWSGLVCYEFVLGKPPFEANTYQTYKRSRVEFTFPDFVTGARDLISRLLLKHNP 369
 DB 254 VDLWCIGVLGYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTCAQDLISKLLRHNP 313
 QY 370 QRPMLREYVLEHFWITANSK---PSNCON 395
 DB 314 ERLPLAQVSAHPWVRANGRRVLPPSALQS 342
 RESULT 26
 AAY22475
 ID AAY22475 standard; protein; 344 AA.
 XX AAY22475;
 AC AAY22475;
 XX 29-SEP-1999 (first entry)
 DT 29-SEP-1999 (first entry)
 XX Human AUR1 protein sequence.
 DE Human AUR1 protein sequence.
 KW AUR1; AUR2; human; AUR modulator; cancer; glioma; medullablastoma;
 KW chondrosarcoma; pancreatic tumour; proliferative disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO9937788-A2.
 PD 29-JUL-1999.
 XX 21-JAN-1999; 99WO-US001283.
 PR 22-JAN-1998; 98US-00012135.
 XX (SUGB-) SUGEN INC.
 PA Plowman GD, Mossie K;
 PI WPI; 1999-458699/38.
 DR N-PSDB; AAX99724.
 XX New nucleic acid encoding human AUR1 and 2 polypeptides, used to identify
 PT specific modulators for treating cancer or for diagnosis.
 PS Claim 11; Page 140-141; 153pp; English.
 CC This sequence is the human AUR1 protein of the invention. The AUR1 and
 CC AUR2 proteins can be used to identify specific modulators of, and to
 CC generate specific antibodies recognising AUR1 and AUR2. The modulators
 CC can be used for treating conditions involving abnormal AUR signal
 CC transduction, specifically cancer (of colon, breast, kidney, ovary,
 CC bladder, head or neck, also glioma, medullablastoma, chondrosarcoma and
 CC pancreatic tumours, particularly of colon (specifically), breast or
 CC kidney). The modulators can also be used for studying their effects in
 CC animal models of proliferative disease. Probes, based on the coding
 CC sequences are used, diagnostically, to detect or quantify AUR mRNA, by
 CC hybridisation or polymerase chain reaction (PCR). The DNA, optionally
 CC mutated, are useful in gene therapy. Ab are used as diagnostic
 CC immunoassay reagents for detecting the proteins
 XX Sequence 344 AA;
 SQ
 Query Match 50.1%; Score 1057.5; DB 2; Length 344;
 Best Local Similarity 63.2%; Pred. No. 3.7e-89;
 Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
 QY 82 TSVPHVSRPLNNTQSKOPL-PSA-----PENNPEELASKQKNVESKK-----RQWA 129
 DB 22 STLPRQVLR-----KEPVTFSALVLMRSRNVQPTAAPGQKWMENSGTDPDLTRHFT 73
 QY 130 LEDFEGRLPGKGFNGVYLAREKQSKFILALKVLFKAOLEKAGVHQHRLRREVEIQSHLR 189
 DB 74 IDDFEIGRLPGKGFNGVYLAREKSHFIVALKVLFKSIQIEKGEVHQHRLREIEIOAHLH 133

QY 190 HPMILRYGYFHDATRVYILEYAPLGTGVYRELQKLSKFDEQRTATVITELANALSYCHS 249
 DB 134 HPMILRYNYFYDRRIYILEYAPRGELYKELOKSCCTFDEQRTATIMEELADALMYCHG 193
 QY 250 KRVIHRIKPEENLLIGSAGELKIADFGWSVHAPSSRRTLLCGTLDYLPPEMIGRMHDEK 309
 DB 194 KRVIHRIKPEENLLIGLKGELKIADFGWSVHAPSLRRTKTCGTLDTYLPPEMIGRMHNEK 253
 QY 310 VDLWSGLVLCYEFVLEHPPPEANTYQETVKRISRVETFPDFVTEGARDLISRLKHNP 369
 DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFASVPTGAQDLISKLRHNP 313
 QY 370 QRPMLREVLEHPWITANSK---PSNCON 395
 DB 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 27
 AAG67615
 ID AAG67615 standard; protein; 344 AA.
 XX AC AAG67615;
 XX DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of a human protein.
 XX KW Human; protein kinase; protein phosphatase; signal transduction.
 XX OS Homo sapiens.
 XX PN WO200109316-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-JP005061.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 18-OCT-1999; 99US-0159590P.
 XX PR 11-JAN-2000; 2000JP-00118776.
 XX PR 17-FEB-2000; 2000US-0183322P.
 XX PR 02-MAY-2000; 2000JP-00183767.
 XX PR 09-JUN-2000; 2000JP-00241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX DR WPI; 2001-570286/64.
 XX PT New genes encoding proteins with protein kinase/protein phosphatase
 PT activity, useful in the diagnosis and treatment of diseases.
 XX PS Example 4; Page 97-100; 233pp; Japanese.
 XX CC The specification describes human protein kinase/protein phosphatases. It
 CC is expected that the protein kinase/protein phosphatase gene participates
 CC in signal transduction in cells. The protein kinase/protein phosphatase
 CC polypeptides and polynucleotides are useful for developing diagnostics
 CC and treatment agents for human and animal diseases. The protein
 CC kinase/protein phosphatase polypeptides are useful as target molecules in
 CC designing novel drugs. The protein kinase/protein phosphatase
 CC polynucleotides are useful as a source of probes and primers, which may
 CC be used to isolate homologous sequences. The present sequence represents
 CC a human protein, which is used in the course of the invention
 XX SQ Sequence 344 AA;

Query Match 50.1%; Score 1057.5; DB 4; Length 344;
 Best Local Similarity 63.2%; Pred. No. 3.7e-89;
 Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSPLNNTQSKOPL-PSA-----PENPEBELASKQKNSKK-----ROWA 129
 DB 22 STLQPVLR-----KEFVTPSALVLMRSRNVQPTAAPGQKVMENSSGTPIILTRHFT 73
 QY 130 LEDFETRPLGKGFKNVYLAREKQSKFILAKVLFKAQLEKAGVEHQLRREVEIQSHLR 189
 DB 74 IDDFELGRPLGKGFKNVYLAREKQSKSHFIVALKVLFKSQIEKGEVHQLRREVEIQALH 133
 QY 190 HPMILRYGYFHDATRVYILEYAPLGTGVYRELQKLSKFDEQRTATVITELANALSYCHS 249
 DB 134 HPMILRYNYFYDRRIYILEYAPRGELYKELOKSCCTFDEQRTATIMEELADALMYCHG 193
 QY 250 KRVIHRIKPEENLLIGSAGELKIADFGWSVHAPSSRRTLLCGTLDYLPPEMIGRMHDEK 309
 DB 194 KRVIHRIKPEENLLIGLKGELKIADFGWSVHAPSLRRTKTCGTLDTYLPPEMIGRMHNEK 253
 QY 310 VDLWSGLVLCYEFVLEHPPPEANTYQETVKRISRVETFPDFVTEGARDLISRLKHNP 369
 DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFASVPTGAQDLISKLRHNP 313
 QY 370 QRPMLREVLEHPWITANSK---PSNCON 395
 DB 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 28
 AAG67436
 ID AAG67436 standard; protein; 344 AA.
 XX AC AAG67436;
 XX DT 26-NOV-2001 (first entry)
 XX DE Amino acid sequence of a human polypeptide.
 XX KW Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 XX OS Homo sapiens.
 XX PN WO200109345-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-JP005060.
 XX PR 29-JUL-1999; 99JP-00248036.
 XX PR 18-OCT-1999; 99US-0159590P.
 XX PR 11-JAN-2000; 2000JP-00118776.
 XX PR 17-FEB-2000; 2000US-0183322P.
 XX PR 02-MAY-2000; 2000JP-00183767.
 XX PA (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 Senoo C, Nezu J;
 WPI; 2001-564736/63.
 New genes encoding protein kinase and protein phosphatase, useful for
 identifying modulators which can be used to treat human or animal
 disorders associated with the expression or function of these enzymes.
 Example 4; Page 199-201; 336pp; Japanese.
 The specification describes human protein kinase/protein phosphatases.
 The polypeptides are expected to participate in signal transduction in
 cells. The kinase phosphatases are connected with intracellular
 signalling pathways. Antisense oligonucleotides and compounds identified
 by screening (agonists or antagonists) can be used to treat human or
 animal disorders associated with the expression or function of the

CC	protein. In addition, the polypeptides may be used as target molecules	XX	The present invention describes a method for detecting a bladder cancer-
CC	for drug development. The present sequence represents a polypeptide, used	CC	associated transcript in a cell from a patient. The method comprises
CC	in the course of the invention	CC	contacting a biological sample from the patient with a polynucleotide
XX		CC	that selectively hybridizes to a sequence that is 80 % identical to a
SQ	Sequence 344 AA;	CC	table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
		CC	encode the human bladder cancer-associated proteins given in ABR48146 to
		CC	ABR48242). Bladder cancer-associated sequences from the present invention
		CC	have cytostatic activities, and can be used in antisense gene therapy and
		CC	in vaccine production. The method can be used for detecting a bladder
		CC	cancer-associated transcript in a cell from a patient. The method is
		CC	useful in diagnosing or treating bladder cancer and in screening for
		CC	compounds that modulate bladder cancer, such as hormones or antibodies.
		CC	The nucleic acid molecules from the present invention may be used in
		CC	various screening and diagnostic methods, and for gene therapy, vaccine
		CC	and/or antisense/inhibition applications
XX		XX	
SQ	Sequence 344 AA;	SQ	Sequence 344 AA;
			Query Match 50.1%; Score 1057.5; DB 6; Length 344;
			Best Local Similarity 63.2%; Pred. No. 3.7e-89;
			Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY	82 TSVPHVPSRLNNTOKSKOPL-PSA-----PENNPEELASKOKNERSKK-----ROWA 129	QY	82 TSVPHVPSRLNNTOKSKOPL-PSA-----PENNPEELASKOKNERSKK-----ROWA 129
DB	22 STLPOQVLR-----KEPVTPEALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73	DB	22 STLPOQVLR-----KEPVTPEALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY	130 LEDFETGRPLGKGFNGVYLAREKSKFIALKVLKFAOLEKAGVHQRRREVEIQSHLR 189	QY	130 LEDFETGRPLGKGFNGVYLAREKSKFIALKVLKFAOLEKAGVHQRRREVEIQSHLR 189
DB	74 IDDFEIGRPLGKGFNGVYLAREKSKHFIVALKVLFKSIQIEKGEVHQRRREIEIQAHLLH 133	DB	74 IDDFEIGRPLGKGFNGVYLAREKSKHFIVALKVLFKSIQIEKGEVHQRRREIEIQAHLLH 133
QY	190 HPNILRLYGFHDATRVYLILEYAPLGTVYVRELQKLSKFEQRTATYITELANALSYCHS 249	QY	190 HPNILRLYGFHDATRVYLILEYAPLGTVYVRELQKLSKFEQRTATYITELANALSYCHS 249
DB	134 HPNILRLYNYFYDRRIYLLILEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193	DB	134 HPNILRLYNYFYDRRIYLLILEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193
QY	250 KRVIHRIKIPENLLLSAGELKIADFGWSVHAPSSRRITLCGTLDYLPPEMIEGRMHDEK 309	QY	250 KRVIHRIKIPENLLLSAGELKIADFGWSVHAPSSRRITLCGTLDYLPPEMIEGRMHDEK 309
DB	194 KKVIHRIKIPENLLLSAGELKIADFGWSVHAPSSRRITLCGTLDYLPPEMIEGRMHNEK 253	DB	194 KKVIHRIKIPENLLLSAGELKIADFGWSVHAPSSRRITLCGTLDYLPPEMIEGRMHNEK 253
QY	310 VDLWSLGVLCYELVGLKPPPEANTYQETVKRISRVEFTFPDFVTEGARDLISRLLKHNS 369	QY	310 VDLWSLGVLCYELVGLKPPPEANTYQETVKRISRVEFTFPDFVTEGARDLISRLLKHNS 369
DB	254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVKVDLKPFPASVPTGAQDLISKLLRHNS 313	DB	254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVKVDLKPFPASVPTGAQDLISKLLRHNS 313
QY	370 QRPMLREVLEHPWITANSKK---PSNCQN 395	QY	370 QRPMLREVLEHPWITANSKK---PSNCQN 395
DB	314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342	DB	314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
			RESULT 30
			ABU56641
ID	ABU56641 standard; protein; 344 AA.	ID	ABU56641 standard; protein; 344 AA.
XX		XX	
AC	ABU56641;	AC	ABU56641;
XX		XX	
DT	02-APR-2003 (first entry)	DT	02-APR-2003 (first entry)
XX		XX	
DE	Lung cancer-associated polypeptide #234.	DE	Lung cancer-associated polypeptide #234.
XX		XX	
KW	Lung cancer-associated polypeptide; cytostatic; emphysema;	KW	Lung cancer-associated polypeptide; cytostatic; emphysema;
KW	antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;	KW	antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;	KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;	KW	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.	KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX		XX	
OS	Unidentified.	OS	Unidentified.
XX		XX	
PN	WO200286443-A2.	PN	WO200286443-A2.
XX		XX	
PD	31-OCT-2002.	PD	31-OCT-2002.
XX		XX	
PF	18-APR-2002; 2002WO-US012476.	PF	18-APR-2002; 2002WO-US012476.
XX		XX	
PR	18-APR-2001; 2001US-0284770P.	PR	18-APR-2001; 2001US-0284770P.

```
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
PA
XX
XX Aziz N, Murray R;
PI
XX WPI; 2003-093161/08.
DR N-PSDB; ABX76370.
DR
XX
XX
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 371; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridizes
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
XX Sequence 344 AA;
XX
XX Query Match 50.1%; Score 1057.5; DB 6; Length 344;
XX Best Local Similarity 63.2%; Pred. No. 3.7e-89;
XX Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 82 TSVPHVPSRLNNTQKSKOPL-PSA-----PENNPEELASKQKNESKK-----RQWA 129
DB 22 STLQORVLR-----KEPVTFSALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRLPGKGFNGVYLAREKSKFTLALKVLFKAOLEKAGVHQHRRVEIOHSLR 189
DB 74 IDDFEIGRLPGKGFNGVYLAREKSKHFIVALKVLFKSKIEKEGVHQHRRREIOAHHL 133
QY 190 HPNILRLGYFHDATRVYLILEYAPLGTVYRELQKLSKDEQRTATYITELANALSYCHS 249
DB 134 HPNILRLYNYFYDRRRYILILEYAPRGELYKELQSKCTFDEQRTATIMELADALMYCHG 193
QY 250 KRVIIHRDIKPNLLIGSAGELKIADFGWSVHAPSRRRTTLCTGLDYLPEMIEGRMHDEK 309
DB 194 KRVIIHRDIKPNLLIGLKGELKIADFGWSVHAPSLRRKTCWGLDYLPEMIEGRMHDEK 253
QY 310 VDLMSGLVLCYEPFLVGKPPFEANTYQETIKRISRVFTFPDFVTEGARDLISRLKHNPS 369
DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKEFPASVPTGAQDLISKLREHNS 313
QY 370 QRPMLREVLEHPWITANSK---PSNCQN 395
DB 314 ERLPLAQVSAHPWVRANSRVLPPSALQS 342
XX
XX RESULT 31
XX ABR92152
```

```
ID ABR92152 standard; protein; 344 AA.
XX
AC ABR92152;
XX
XX 10-SEP-2003 (first entry)
DT
DE Human cervical cancer cell marker protein SEQ ID NO:214.
XX
XX Human cervical cancer; cervical cancer marker; cancer therapy;
KW detection; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO2002101075-A2.
PN
XX 19-DEC-2002.
PD
XX 12-JUN-2002; 2002WO-US018638.
PF
XX 13-JUN-2001; 2001US-0298155P.
PR 13-JUN-2001; 2001US-0298159P.
PR 14-NOV-2001; 2001US-0335936P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI Gannavarapu M, Glatt K, Hoersch S;
XX
XX WPI; 2003-156967/15.
DR N-PSDB; ACF12935.
DR
XX
XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
XX Claim 4; Page 366-367; 386pp; English.
XX
XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterising,
CC preventing and treating human cervical cancers. (I) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
XX Sequence 344 AA;
XX
XX Query Match 50.1%; Score 1057.5; DB 6; Length 344;
XX Best Local Similarity 63.2%; Pred. No. 3.7e-89;
XX Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 82 TSVPHVPSRLNNTQKSKOPL-PSA-----PENNPEELASKQKNESKK-----RQWA 129
DB 22 STLQORVLR-----KEPVTFSALVMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRLPGKGFNGVYLAREKSKFTLALKVLFKAOLEKAGVHQHRRVEIOHSLR 189
DB 74 IDDFEIGRLPGKGFNGVYLAREKSKHFIVALKVLFKSKIEKEGVHQHRRREIOAHHL 133
QY 190 HPNILRLGYFHDATRVYLILEYAPLGTVYRELQKLSKDEQRTATYITELANALSYCHS 249
DB 134 HPNILRLYNYFYDRRRYILILEYAPRGELYKELQSKCTFDEQRTATIMELADALMYCHG 193
QY 250 KRVIIHRDIKPNLLIGSAGELKIADFGWSVHAPSRRRTTLCTGLDYLPEMIEGRMHDEK 309
```


PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
DR WPI; 2003-468649/44.
DR N-PSDB; ADN38884.
XX
PT Determining the presence or absence of a pathological cell in a patient.
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 203; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 344 AA;

Query Match 50.1%; Score 1057.5; DB 7; Length 344;
Best Local Similarity 63.2%; Pred. No. 3.7e-89;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSPLNNTQSKOPL-PSA-----PENNPEELASKOKNESKK-----RQWA 129
DB 22 STLPQRLVLR-----KEPVTFSALVMSRSNVQPTAAPGQKVMNSSGTDPDLTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKLVFKAQLEKAGVHQHQRREVEIQSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKSKFHFVAVKLVFQSKIEKGVHQHQRREVEIQSHLR 133

QY 190 HPNLRLYGYFHDATRVYLILEYAPVGTVYRELOKLSKFDEQRTATYITELANALSYCHS 249
DB 134 HPNLRLYNYFYDRIIRYILVYAPRGELYKELQSKCTFDEQRTATIMEELADALMYCHG 193

QY 250 KRVIHRDIKPNILLLGAGELKTIADFGWSVHAPSSRRRTTCGTLDTLVPPEMIEGRHDEK 309
DB 194 KKVHHRDIKPNILLLGAGELKTIADFGWSVHAPSSRRRTTCGTLDTLVPPEMIEGRHNEK 253

QY 310 VDLWSLGLVLCYEFVLGKPPPEANTYORTYKRISRVFTFPDFTVEGARDLISLLKHNP 369
DB 254 VDLWCGLVLCYELLGNPPPEASHNETYRIYKVDLKPASVPTGAQDLISKLRHNP 313

QY 370 QRMPLREVLHPHWTANSSK---PSNCON 395
DB 314 ERLPLAQVSAHPVWVANSRVLPSALQS 342

RESULT 34
ADN95464
ID ADN95464 standard; protein; 344 AA.
XX
AC ADN95464;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human BEC/LEC-related protein sequence SeqID387.
XX
KW growth; differentiation; blood endothelial cell; BEC;
KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;

KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
KW inflammatory disease; cancer metastasis; lymphatic system; human.
OS Homo sapiens.
PN WO2003080640-A1.
XX 02-OCT-2003.
PD
PF 07-MAR-2003; 2003WO-US006900.
PR
XX 07-MAR-2002; 2002US-0363019P.
XX (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
DR N-PSDB; ADN95465.
XX
PS Example 1; SEQ ID NO 387; 176pp; English.
XX
CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprises contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
CC composition comprising a lymphatic growth agent selected from VEGF-C or
CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
CC the development of compounds with an antiangiogenic, cytostatic,
CC vasotropic or antiinflammatory activity or for gene therapy. The method
CC is useful in modulating the growth or differentiation of blood
CC endothelial cells or lymphatic endothelial cells, in treating hereditary
CC lymphoedema, in screening for an endothelial cell disorder or
CC predisposition to the disorder or in monitoring the efficacy or toxicity
CC of a drug on endothelial cells. The agent is useful in manufacturing a
CC medicament for the differential modulation of blood vessel endothelial
CC cell or lymphatic vessel endothelial cell growth or differentiation. The
CC lymphatic growth agent may also be used in manufacturing a medicament for
CC the treatment of hereditary lymphoedema resulting from a mutation in a
CC LEC gene or of other diseases involving the lymphatic vessels, such as
CC various inflammatory diseases and cancer metastasis via the lymphatic
CC system. The present sequence is that of a human LEC/BEC differentially
CC expressed protein which is related to the method of the invention. Note:
CC This sequence does not appear in the specification but was obtained by
CC the indexer using the source data given in table 14 of the specification.
XX
SQ Sequence 344 AA;

Query Match 50.1%; Score 1057.5; DB 7; Length 344;
Best Local Similarity 63.2%; Pred. No. 3.7e-89;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVPSPLNNTQSKOPL-PSA-----PENNPEELASKOKNESKK-----RQWA 129
DB 22 STLPQRLVLR-----KEPVTFSALVMSRSNVQPTAAPGQKVMNSSGTDPDLTRHFT 73

QY 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKLVFKAQLEKAGVHQHQRREVEIQSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKSKFHFVAVKLVFQSKIEKGVHQHQRREVEIQSHLR 133

QY 190 HPNLRLYGYFHDATRVYLILEYAPVGTVYRELOKLSKFDEQRTATYITELANALSYCHS 249
DB 134 HPNLRLYNYFYDRIIRYILVYAPRGELYKELQSKCTFDEQRTATIMEELADALMYCHG 193

QY 250 KRVIHRDIKPNILLLGAGELKTIADFGWSVHAPSSRRRTTCGTLDTLVPPEMIEGRHDEK 309
DB 194 KKVHHRDIKPNILLLGAGELKTIADFGWSVHAPSSRRRTTCGTLDTLVPPEMIEGRHNEK 253


```
SQ Sequence 344 AA;
Query Match 50.1%; Score 1057.5; DB 8; Length 344;
Best Local Similarity 63.2%; Pred. No. 3.7e-89;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVSRPLNNTQSKQPL-PSA-----PENNPEELASKQKNESSK-----RQWA 129
DB 22 STLPQVRVLR-----KEPVTSPALVMSRSNVQPTAAPQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRREVEIOSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKGEVHQLRREVEIOAHLH 133
QY 190 HPMILRLYGVFHDATRVYLILEYAPLGTVTYRELOKLSKDEQRTATYITELANALSYCHS 249
DB 134 HPMILRLYNYFYDRRIYLIILEYAPRGELYKELQKSCFDEQRTATIMEELADALMYCHG 193
QY 250 KRVIHREDIKPENLLLSAGELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHDEK 309
DB 194 KKVIHREDIKPENLLLSAGELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253
QY 310 VDLWSLGVLCYELVGNPPFESASHNETYRIRVKVDLKFPPASVPTGAQDLISKLLRHNS 369
DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVKVDLKFPPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHPWITANSK---PSNCQN 395
DB 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 37
ABM81826
ID ABM81826 standard; protein; 344 AA.
XX
AC ABM81826;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT). polypeptide PRO70812, SEQ:4700.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI: 2004-347921/32.
DR N-PSDB; ACN40117.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 4700; 7273pp; English.
XX
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CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 344 AA;
Query Match 50.1%; Score 1057.5; DB 8; Length 344;
Best Local Similarity 63.2%; Pred. No. 3.7e-89;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 82 TSVPHVSRPLNNTQSKQPL-PSA-----PENNPEELASKQKNESSK-----RQWA 129
DB 22 STLPQVRVLR-----KEPVTSPALVMSRSNVQPTAAPQKVMENSSGTPDILTRHFT 73
QY 130 LEDFEIGRPLGKGFNGVYLAREKQSFILAKVLFKAQLEKAGVEHQLRREVEIOSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKGEVHQLRREVEIOAHLH 133
QY 190 HPMILRLYGVFHDATRVYLILEYAPLGTVTYRELOKLSKDEQRTATYITELANALSYCHS 249
DB 134 HPMILRLYNYFYDRRIYLIILEYAPRGELYKELQKSCFDEQRTATIMEELADALMYCHG 193
QY 250 KRVIHREDIKPENLLLSAGELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHDEK 309
DB 194 KKVIHREDIKPENLLLSAGELKIADFGWSVHAPSLRRTKTCGTLDYLPPEMIEGRMHNEK 253
QY 310 VDLWSLGVLCYELVGNPPFESASHNETYRIRVKVDLKFPPASVPTGAQDLISKLLRHNS 369
DB 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVKVDLKFPPASVPTGAQDLISKLLRHNS 313
QY 370 QRPMLREVLEHPWITANSK---PSNCQN 395
DB 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342

RESULT 38
ABR61580
ID ABR61580 standard; protein; 344 AA.
XX
AC ABR61580;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human HeAIRK-2 (Auroa A) protein.
XX
KW RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; HeAIRK-2;
KW Auroa A.
XX
OS Homo sapiens.
XX
PN WO2003087395-A2.
XX
PD 23-OCT-2003.
XX
PS 15-APR-2003; 2003WO-IB002972.
XX
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PR 15-APR-2002; 2002US-0372483P.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX Garbay C, Gigoux V, Canonis J, L'hoete S, Samson J;
XX WPI; 2003-845340/78.
DR N-PSDB; ACF58069.
XX Identifying anti-tumoral compounds, comprises determining the capacity of
PT a compound to inhibit interaction between RasGAP and Drosophila
PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
PT aurora binding protein.
XX Disclosure; Page 62-63; Opp; English.
XX The invention relates to identifying a biologically active compound with
CC anti-tumoral properties, where the compound is studied for its capacity
CC to inhibit the interaction between: (a) RasGAP and the Drosophila
CC melanogaster Aurora kinase or an orthologue of the kinase, or its
CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
CC protein and the D. melanogaster Aurora kinase or an orthologue of the
CC kinase, or its fragment. The method is useful for identifying anti-
CC tumoral agents. The present sequence represents a human HsAURK-2 (Aurora
CC A) protein, an orthologue of the D. melanogaster Aurora kinase
XX Sequence 344 AA;
SQ
Query Match 50.1%; Score 1056.5; DB 7; Length 344;
Best Local Similarity 63.2%; Pred. No. 4.6e-89;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 82 TSVPHPVPLNNTQSKOPL-PSA-----PENNPEELASKQNESSKK-----RQWA 129
DB 22 STLPQRLVLR-----KEPTVPSALVMSRSNVQPTAAPGGQKVMSSGTPDILTRHFT 73
QY 130 LEDEFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQRLRREVEIQSHLR 189
DB 74 IDDFEIGRPLGKGFNGVYLAREKQSFILALKVLFKAQLEKAGVEHQRLRREVEIQSHLR 133
QY 190 HPNILRLYGVFHDATRVYLILEVAPLGTVYRELOKLSKDFEORTATYITELANALSYCHS 249
DB 134 HPNILRLYNYFYDRRIYVILEVAPRGELYKELQKSCTFDEORTATIMEELADALMYCHG 193
QY 250 KRVIHRIKPEENLLGASGELKTDPCWSVHAPSRRRTTLTDLVLPPEMIGRMHDEK 309
DB 194 KRVIHRIKPEENLLGKELKTDPCWSVHAPSRLRRTKTCGTLVLPPEMIGRMHNEK 253
QY 310 VDLWSLGLVLCYEFVLGKPPPEANTYQETVKRISRVVEFTFPDFTEGARDLISRLKHNPS 369
DB 254 VDLWCIGVLCYELLVGNPPPEASHNETYRIVKVDLKFPSVPMGAQDLISKLRRNPS 313
QY 370 QRPMLREVLEHPWITANSSK---PSNCON 395
DB 314 ERLPLAQSAHPWVRANSRRVLPESALQS 342
RESULT 39
AAW99783
ID AAW99783 standard; protein; 343 AA.
XX
XX AAW99783;
XX
XX 07-JUN-1999 (first entry)
XX
XX Rat AIM-1.
XX
XX Rat; AIM-1; aurora and IPL-1 like midbody-associated protein kinase;
XX cell cycle regulating protein; serine-threonine kinase;
XX cell proliferation; cancer.
XX
XX Rattus sp.
XX
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PN WO9909160-A1.
XX
XX 25-FEB-1999.
XX
XX 17-AUG-1998; 98WO-JP003641.
XX
XX 15-AUG-1997; 97JP-00235371.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tatsuka M, Terada Y;
XX WPI; 1999-181033/15.
DR N-PSDB; AAX19715.
XX
XX DNA encoding cell cycle-regulating protein, aurora and IPL-1 like midbody
PT associated protein kinase AIM-1 - useful for treatment of diseases
PT associated with abnormal proliferation of cells e.g. cancers.
XX
XX Claim 1; Page 31-35; 44pp; Japanese.
XX
XX The present sequence represents rat aurora and IPL-1 like midbody-
CC associated protein kinase, designated AIM-1. AIM-1 protein inhibitors
CC obtained can be used as remedies for treatment of diseases associated
CC with abnormal cell proliferation, e.g. cancers. The genes and AIM-1
CC proteins can be applied in the screening of substances with serine-
CC threonine kinase inhibitory activity. Hybridised oligonucleotides and
CC peptide nucleic acids can be used to the inhibit expression of the AIM-1
CC proteins
XX
XX Sequence 343 AA;
SQ
Query Match 49.8%; Score 1050; DB 2; Length 343;
Best Local Similarity 57.6%; Pred. No. 1.8e-88;
Matches 204; Conservative 51; Mismatches 73; Indels 26; Gaps 4;
QY 36 PLFVNSGQQRVLCPSNSSQVRPLQAQKLVSSHKPVQNKQKQKQLQATSVPHVPSRPLNNT 95
DB 9 PWPYSGKTSQSL--NTLPQRV-LRKEPAVTPAQAALMNR-----SNS 47
QY 96 QKSQKPLPAPENNPPEELASKQNEESKKQWALEDFEIGRPLGKGFNGVYLAREKQS 155
DB 48 QSTAVFGQKLTENKGATALQSQ-----SRQPTIDNFEIGRPLGKGFNGVYLAREKKS 102
QY 156 KFTLALKVLFKAQLEKAGVEHQRLRREVEIQSHLRHPNILRLYGVFHDATRVYLILEYAPL 215
DB 103 RIVALKILFKSQIEKEGVEHQRLRREIEQAHLKHPNILQLNYFYDQQRVYLILEYAPR 162
QY 216 GTVYRELOKLSKDFEORTATYITELANALSYCHSKRVIHRDIKPNELLGSGAGELKIADF 275
DB 163 GELYKELQKSGTFDEORTATIMEELSDALMYCHKKKVIHRDIKPNELLGLQELKIADF 222
QY 276 GWSVHAPSRRRTTLGTLVLPPEMIGRMHDEKVDLWSLGLVLCYEFVLGKPPPEANTYQ 335
DB 223 GWSVHAPSRLRRTKTCGTLVLPPEMIGRMHDEKVDLWCIGVLCYELMVGNNPFPFSPHS 282
QY 336 ETVKTRISRVVEFTFPDFVTEGARDLISRLKHNPSQRPMLREVLEHPWITANSSK 389
DB 283 ETVRIRIVVDLKFPPSPMPLGAKDLISKLKHNPSQRLPLEQVSAHPWVRANSRR 336
RESULT 40
AAV27052
ID AAY27052 standard; protein; 347 AA.
XX
XX AAY27052;
XX
XX 08-OCT-1999 (first entry)
XX
XX Human protein kinase (HPKM)-1 (clone ID 2940).
XX
XX Human protein kinase molecule; HPKM; human; protein kinase;
XX phosphate group; cancer; immune disorder.
XX
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JC5974
 aurora-related kinase 1 (EC 2.7.-.-) - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 16-Aug-2004
 C:Accession: JC5974
 R:Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; Jenk
 Biochem. Biophys. Res. Commun. 244, 285-292, 1998
 A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
 A:Reference number: JC5974; MUID:98183439; PMID:9514916
 A:Accession: JC5974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-403 <SH1>
 A:Cross-references: GB:AF008551
 C:Superfamily: protein kinase homology
 C:Keywords: phosphotransferase
 F:131-383/Domain: protein kinase homology <KIN>

Search completed: June 20, 2005, 20:07:58
Job time : 37.5274 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:46:50 ; Search time 122.495 Seconds

(without alignments)

1086.128 Million cell updates/sec

Title: US-10-734-126-3

Perfect score: 1809

Sequence: 1 MDAQENSYWPYGRQTAPSG.....PWVRNSRRVLPPSALQSV 344

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 56

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 49%

Maximum Match 100%

Listing first 65000 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1809	100.0	344	2 AAW18083	Aay22475 Human Aur
2	1809	100.0	344	2 AAY22475	Aay22475 Human Aur
3	1809	100.0	344	4 AAG67615	Aag67615 Amino aci
4	1809	100.0	344	4 AAG67436	Aag67436 Amino aci
5	1809	100.0	344	6 ABR48188	Abr48188 Human bla
6	1809	100.0	344	6 ABUS6641	Abus6641 Lung canc
7	1809	100.0	344	6 ABR32152	AbR32152 Human cer
8	1809	100.0	344	7 ADB80537	AdB80537 Ovarian c
9	1809	100.0	344	7 ADN38885	Adn38885 Cancer/an
10	1809	100.0	344	7 ADN95464	Adn95464 Human BEC
11	1809	100.0	344	8 ADK67718	Adk67718 Human mod
12	1809	100.0	344	8 ADQ89834	Adq89834 Antagonis
13	1809	100.0	344	8 ABM81826	Abm81826 Tumour-as
14	1803	99.7	344	7 ABR61580	Abr61580 Human Hsa
15	1797.5	99.4	347	2 AAY27052	Aay27052 Human pro
16	1797.5	99.4	347	6 ABUS7643	Abus7643 Different
17	1770.5	97.9	343	8 ADM72221	Adm72221 Human TAS
18	1529	84.5	312	7 ADC10236	Adc10236 Human NOV
19	1520.5	84.1	343	2 AAW99783	Aaw99783 Rat AIM-1
20	1201	66.4	275	7 ABR61581	Abr61581 Human Hsa
21	1201	66.4	275	8 ADK67719	Adk67719 Human mod
22	1181	65.3	355	5 ABUS6047	Abus6047 Human NOV
23	1171.5	64.8	356	8 ADN61745	Adn61745 Human nov
24	1124	62.1	320	8 ADO57331	Ado57331 Kidney de
25	1057.5	58.5	403	2 AAW18084	Aaw18084 Human Aur

ALIGNMENTS

RESULT 1

AAW18083
ID AAW18083 standard; protein; 344 AA.

XX AC AAW18083;

XX XX

DT 07-SEP-1997 (first entry)

XX XX

DE Human Aurora-1.

KW Aurora-1; AUR-1; signal transduction; protein kinase; tumour; cancer; protein kinase; gene therapy; diagnosis; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..74

FT Domain /label= N-terminal_domain

FT Domain 74..344

FT Modified-site 232

FT /label= Phosphorylation

FT /note= "cAMP-dependent protein kinase phosphorylation site conserved in AUR-2 and yeast and Drosophila homologues"

FT Misc-difference 265

PN /note= "deduced residue from some cDNA clones is Gly"

XX WO9722702-A1.

PD 26-JUN-1997.

XX 25-NOV-1996;

PF 96WO-US018859.

PR 18-DEC-1995;

PR 14-AUG-1996;

XX 95US-0008809P.

XX 96US-0023943P.

26	1057.5	58.5	403	2 AAY22476	Aay22476 Human Aur
27	1057.5	58.5	403	4 AAG67614	Aag67614 Amino aci
28	1057.5	58.5	403	4 AAG67435	Aag67435 Amino aci
29	1057.5	58.5	403	6 ABP97367	Abp97367 Human ser
30	1057.5	58.5	403	6 ABP97366	Abp97366 Human ser
31	1057.5	58.5	403	6 ABR48160	Abr48160 Human bla
32	1057.5	58.5	403	7 ABR61840	Abr61840 Human ser
33	1057.5	58.5	403	7 ADN39888	Adn39888 Cancer/an
34	1057.5	58.5	403	8 ADE15337	Adel5337 Truncated
35	1057.5	58.5	403	8 ADH59556	Adh59556 Monoclonal
36	1057.5	58.5	403	8 ADK67720	Adk67720 Human mod
37	1057.5	58.5	403	8 ADM72205	Adm72205 Human TAS
38	1057.5	58.5	403	8 ADQ89832	Adq89832 Antagonis
39	1057.5	58.5	403	8 ADR05174	Adr05174 Human GTP
40	1057.5	58.5	420	5 ABR41958	Abp41958 Human ova
41	1050.5	58.1	319	6 ABP97470	Abp97470 Truncated
42	1050.5	58.1	403	7 ADJ31727	Adj31727 Human mit
43	1045.5	57.8	402	7 ABR61579	Abr61579 Human Hsa
44	1045.5	57.8	402	7 ADQ89969	Adq89969 Human can
45	1043.5	57.7	309	6 ABP97472	Abp97472 Truncated
46	1041.5	57.6	300	6 ABP97473	Abp97473 Truncated
47	966	53.4	403	5 AAO18740	Aao18740 Human NOV
48	940	52.0	294	8 ADJ49242	Adj49242 Oil-assoc
49	937	51.8	294	8 ADJ49602	Adj49602 Oil-assoc
50	934.5	51.7	295	8 ADJ48641	Adj48641 Oil-assoc
51	933.5	51.6	298	8 ADJ48640	Adj48640 Oil-assoc
52	921.5	50.9	282	8 ADJ49236	Adj49236 Oil-assoc
53	918	50.7	368	8 ADJ48378	Adj48378 Maize oil
54	917.5	50.7	418	8 ADJ48815	Adj48815 Oil-assoc
55	908	50.2	298	8 ADJ48546	Adj48546 Oil-assoc
56	906	50.1	432	8 ADJ50416	Adj50416 Oil-assoc


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PA (SUGEN-) SUGEN INC.
XX Plowman GD, Mossie KG;
XX WPI; 1997-341693/31.
DR N-PSDB; AAT67289.
XX Aurora-1 and Aurora-2 and related genes - useful in tumour gene therapy.
PT Claim 3; Page 82-83; 98pp; English.
XX Novel human proteins, termed Aurora-1 (AAW18083) and Aurora-2 (AAW18084)
CC (AUR-1 and AUR-2), are related serine/threonine kinases with short N-
CC terminal extensions that appear to be involved in cancer and/or signal
CC transduction disorders. Their amino acid sequences were deduced from
CC pancreatic tumour cDNA clones (AA167289- 90). AUR-1 and AUR-2 appear to
CC regulate nuclear division, with disruption of their signaling resulting
CC in polyploid cells. AUR-1 RNA is broadly expressed in rapidly dividing
CC cells from normal and tumour tissues. AUR polypeptides can be expressed
CC in host cells and used to raise diagnostic antibodies and to screen for
CC compounds that interact with AUR-1 and/or AUR-2
XX Sequence 344 AA;
SQ
Query Match 100.0%; Score 1809; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.8e-186;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWYGRQTAPSGSLSTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKVMEN 60
DB 1 MAQKENSYPWYGRQTAPSGSLSTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKVMEN 60
QY 61 SSGTDPILTRHTTIDDFTGRPLGKFGNVYLAREKSHFIVALKVLFKSOIEKEGVH 120
DB 61 SSGTDPILTRHTTIDDFTGRPLGKFGNVYLAREKSHFIVALKVLFKSOIEKEGVH 120
QY 121 QLRRETEIQAHLHPNLLRYNYFYDRRRIYLILEYAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETEIQAHLHPNLLRYNYFYDRRRIYLILEYAPRGELYKELQKCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGELKIADFGWSVHAPSLARKTWCGLDYL 240
DB 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGELKIADFGWSVHAPSLARKTWCGLDYL 240
QY 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPESASHNETYRRIYKVDLKFPASVPTGA 300
DB 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPESASHNETYRRIYKVDLKFPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
RESULT 2
AAY22475
ID AAY22475 standard; protein; 344 AA.
XX AAY22475;
XX AAY22475;
XX 29-SEP-1999 (first entry)
XX Human AUR1 protein sequence.
XX AUR1; AUR2; human; AUR modulator; cancer; glioma; medullablastoma;
XX chondrosarcoma; pancreatic tumour; proliferative disease; diagnosis;
XX therapy.
XX Homo sapiens.
XX WO9937788-A2.
XX 29-JUL-1999.
XX
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PF 21-JAN-1999; 99WO-US001283.
XX
PR 22-JAN-1998; 98US-00012135.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Mossie K;
XX
PI WPI; 1999-458699/38.
DR N-PSDB; AAX99724.
DR
XX
XX New nucleic acid encoding human AUR1 and 2 polypeptides, used to identify
PT specific modulators for treating cancer or for diagnosis.
XX
XX Claim 11; Page 140-141; 153pp; English.
XX
XX This sequence is the human AUR1 protein of the invention. The AUR1 and
CC AUR2 proteins can be used to identify specific modulators of, and to
CC generate specific antibodies recognising AUR1 and AUR2. The modulators
CC can be used for treating conditions involving abnormal AUR signal
CC transduction, specifically cancer (of colon, breast, kidney, ovary,
CC bladder, head or neck, also glioma, medullablastoma, chondrosarcoma and
CC pancreatic tumours, particularly of colon (specifically), breast or
CC kidney). The modulators can also be used for studying their effects in
CC animal models of proliferative disease. Probes, based on the coding
CC sequences are used, diagnostically, to detect or quantify AUR mRNA, by
CC hybridisation or polymerase chain reaction (PCR). The DNA, optionally
CC mutated, are useful in gene therapy. Ab are used as diagnostic
CC immunoassay reagents for detecting the proteins
XX
SQ Sequence 344 AA;
Query Match 100.0%; Score 1809; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.8e-186;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWYGRQTAPSGSLSTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKVMEN 60
DB 1 MAQKENSYPWYGRQTAPSGSLSTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKVMEN 60
QY 61 SSGTDPILTRHTTIDDFTGRPLGKFGNVYLAREKSHFIVALKVLFKSOIEKEGVH 120
DB 61 SSGTDPILTRHTTIDDFTGRPLGKFGNVYLAREKSHFIVALKVLFKSOIEKEGVH 120
QY 121 QLRRETEIQAHLHPNLLRYNYFYDRRRIYLILEYAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETEIQAHLHPNLLRYNYFYDRRRIYLILEYAPRGELYKELQKCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGELKIADFGWSVHAPSLARKTWCGLDYL 240
DB 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGELKIADFGWSVHAPSLARKTWCGLDYL 240
QY 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPESASHNETYRRIYKVDLKFPASVPTGA 300
DB 241 PPMIEGRMHNEKVDLWCIGVLCYELLVGNPPESASHNETYRRIYKVDLKFPASVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
RESULT 3
AAG67615
ID AAG67615 standard; protein; 344 AA.
XX AAG67615;
XX AAG67615;
XX 26-NOV-2001 (first entry)
XX Amino acid sequence of a human protein.
XX Human; protein kinase; protein phosphatase; signal transduction.
XX
```

```
OS Homo sapiens.
XX WO200109316-A1.
XX 08-FEB-2001.
XX 28-JUL-2000; 2000WO-JP005061.
XX 29-JUL-1999; 99JP-00248036.
XX 18-OCT-1999; 99US-0159590P.
XX 11-JAN-2000; 2000JP-00118776.
XX 17-FEB-2000; 2000US-0183322P.
XX 02-MAY-2000; 2000JP-00183767.
XX 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Senoo C, Nezu J;
XX WPI; 2001-570286/64.
XX New genes encoding proteins with protein kinase/protein phosphatase
XX activity, useful in the diagnosis and treatment of diseases.
XX Example 4; Page 97-100; 233pp; Japanese.
XX The specification describes human protein kinase/protein phosphatases. It
XX is expected that the protein kinase/protein phosphatase gene participates
XX in signal transduction in cells. The protein kinase/protein phosphatase
XX polypeptides and polynucleotides are useful for developing diagnostics
XX and treatment agents for human and animal diseases. The protein
XX kinase/protein phosphatase polypeptides are useful as target molecules in
XX designing novel drugs. The protein kinase/protein phosphatase
XX polynucleotides are useful as a source of probes and primers, which may
XX be used to isolate homologous sequences. The present sequence represents
XX a human protein, which is used in the course of the invention
XX
XX Sequence 344 AA;
XX
XX Query Match 100.0%; Score 1809; DB 4; Length 344;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-186;
XX Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAQKENSYPWYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQPTAAPGQKWMEN 60
XX |||||
XX 1 MAQKENSYPWYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQPTAAPGQKWMEN 60
XX |||||
XX 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKSIKEGVEH 120
XX |||||
XX 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKSIKEGVEH 120
XX |||||
XX 121 QLRREIEIQAHLHPNLRNLYNYFYDRIIRYLLILEYAPRGELYKELQKSCTFDEQRTATI 180
XX |||||
XX 121 QLRREIEIQAHLHPNLRNLYNYFYDRIIRYLLILEYAPRGELYKELQKSCTFDEQRTATI 180
XX |||||
XX 181 MEELADALMYCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCMGTLDYL 240
XX |||||
XX 181 MEELADALMYCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCMGTLDYL 240
XX |||||
XX 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
XX |||||
XX 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
XX |||||
XX 301 QDLISKLLRHNSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
XX |||||
XX 301 QDLISKLLRHNSERLPLAQVSAHPWVRANSRRVLPSPALQSA 344
XX |||||
XX
XX RESULT 4
XX AAG67436
XX ID AAG67436 standard; protein; 344 AA.
```

```
XX AAG67436;
XX 26-NOV-2001 (first entry)
XX Amino acid sequence of a human polypeptide.
XX Human; protein kinase; protein phosphatase; signal transduction;
XX intracellular signalling pathway.
XX Homo sapiens.
XX WO200109345-A1.
XX 08-FEB-2001.
XX 28-JUL-2000; 2000WO-JP005060.
XX 29-JUL-1999; 99JP-00248036.
XX 18-OCT-1999; 99US-0159590P.
XX 11-JAN-2000; 2000JP-00118776.
XX 17-FEB-2000; 2000US-0183322P.
XX 02-MAY-2000; 2000JP-00183767.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
XX Senoo C, Nezu J;
XX WPI; 2001-564736/63.
XX New genes encoding protein kinase and protein phosphatase, useful for
XX identifying modulators which can be used to treat human or animal
XX disorders associated with the expression or function of these enzymes.
XX Example 4; Page 199-201; 336pp; Japanese.
XX The specification describes human protein kinase/protein phosphatases.
XX The polypeptides are expected to participate in signal transduction in
XX cells. The kinase phosphatases are connected with intracellular
XX signalling pathways. Antisense oligonucleotides and compounds identified
XX by screening (agonists or antagonists) can be used to treat human or
XX animal disorders associated with the expression or function of the
XX protein. In addition, the polypeptides may be used as target molecules
XX for drug development. The present sequence represents a polypeptide, used
XX in the course of the invention
XX
XX Sequence 344 AA;
XX
XX Query Match 100.0%; Score 1809; DB 4; Length 344;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-186;
XX Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAQKENSYPWYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQPTAAPGQKWMEN 60
XX |||||
XX 1 MAQKENSYPWYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQPTAAPGQKWMEN 60
XX |||||
XX 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKSIKEGVEH 120
XX |||||
XX 61 SSGTDPILTRHFTTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKSIKEGVEH 120
XX |||||
XX 121 QLRREIEIQAHLHPNLRNLYNYFYDRIIRYLLILEYAPRGELYKELQKSCTFDEQRTATI 180
XX |||||
XX 121 QLRREIEIQAHLHPNLRNLYNYFYDRIIRYLLILEYAPRGELYKELQKSCTFDEQRTATI 180
XX |||||
XX 181 MEELADALMYCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCMGTLDYL 240
XX |||||
XX 181 MEELADALMYCHGKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCMGTLDYL 240
XX |||||
XX 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
XX |||||
XX 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGA 300
XX |||||
```

QY	301	QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPSALQSV	344
DB	301	QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPSALQSV	344
RESULT 5			
ABR48188			
ID	ABR48188	standard; protein; 344 AA.	
XX	AC	ABR48188;	
XX	DT	12-JUN-2003 (first entry)	
DE	DE	Human bladder cancer associated protein sequence SEQ ID NO:93.	
XX	XX	Human, bladder cancer; cytostatic; gene therapy; vaccine.	
XX	OS	Homo sapiens.	
PN	WO2003003906-A2.		
XX	PD	16-JAN-2003.	
XX	PF	03-JUL-2002; 2002WO-US021338.	
XX	PR	03-JUL-2001; 2001US-0302814P.	
PR	PR	03-AUG-2001; 2001US-0310099P.	
PR	PR	08-NOV-2001; 2001US-0343705P.	
PR	PR	13-NOV-2001; 2001US-0350666P.	
PR	PR	12-APR-2002; 2002US-0372246P.	
XX	PA	(EOSB-) EOS BIOTECHNOLOGY INC.	
XX	PI	Mack DH, Aziz N;	
XX	DR	WPI; 2003-201532/19.	
DR	DR	N-PSDB; ACC51000.	
XX	PT	Detecting a bladder cancer-associated transcript in a cell from a	
PT	PT	patient, comprises contacting a biological sample from the patient with a	
PT	PT	bladder cancer-associated polynucleotide or antibody.	
XX	XX	Claim 10; Page 265; 307pp; English.	
PS	PS	The present invention describes a method for detecting a bladder cancer-	
XX	CC	associated transcript in a cell from a patient. The method comprises	
CC	CC	contacting a biological sample from the patient with a polynucleotide	
CC	CC	that selectively hybridises to a sequence that is 80 % identical to a	
CC	CC	table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059	
CC	CC	encode the human bladder cancer-associated proteins given in ABR48146 to	
CC	CC	ABR48242). Bladder cancer-associated sequences from the present invention	
CC	CC	have cytostatic activities, and can be used in antisense gene therapy and	
CC	CC	in vaccine production. The method can be used for detecting a bladder	
CC	CC	cancer-associated transcript in a cell from a patient. The method is	
CC	CC	useful in diagnosing or treating bladder cancer and in screening for	
CC	CC	compounds that modulate bladder cancer, such as hormones or antibodies.	
CC	CC	The nucleic acid molecules from the present invention may be used in	
CC	CC	various screening and diagnostic methods, and for gene therapy, vaccine	
CC	CC	and/or antisense/inhibition applications	
XX	XX	Sequence 344 AA;	
SQ	SQ	Query Match	100.0%; Score 1809; DB 6; Length 344;
		Best Local Similarity	100.0%; Pred. No. 8.8e-186;
		Matches 344; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MAQKENSYPYGRQTAPSGSLTPQRLRKEPVPSPSALVMSRNVQPTAAGQKVMEN	60
DB	1	MAQKENSYPYGRQTAPSGSLTPQRLRKEPVPSPSALVMSRNVQPTAAGQKVMEN	60
QY	61	SSGTPDILTRHFTIDDFEIGRPLGKGFNVVLAAREKSHFIVALKVLFKSIKEGVEH	120

CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 XX Sequence 344 AA;
 CC
 CC Query Match 100.0%; Score 1809; DB 6; Length 344;
 CC Best Local Similarity 100.0%; Pred. No. 8.8e-186;
 CC Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKWMEN 60
 DB 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKWMEN 60
 QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVH 120
 DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVH 120
 QY 121 QLRREIEIOAHLHPNHLNLYFYDRIYLLILEYAPRGELYKELQKCTFDEQRTATI 180
 DB 121 QLRREIEIOAHLHPNHLNLYFYDRIYLLILEYAPRGELYKELQKCTFDEQRTATI 180
 QY 181 MEELADALMYCHGKVKVHRDIKPNENLLGLKGLKTIADFGWSVHAPSLRRKTCGTLDY 240
 DB 181 MEELADALMYCHGKVKVHRDIKPNENLLGLKGLKTIADFGWSVHAPSLRRKTCGTLDY 240
 QY 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
 DB 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
 QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
 DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
 RESULT 7
 ABR92152
 ID ABR92152 standard; protein; 344 AA.
 XX
 AC ABR92152;
 XX
 DT 10-SEP-2003 (first entry)
 XX
 DE Human cervical cancer cell marker protein SEQ ID NO:214.
 XX
 KW Human; cervical cancer; cervical cancer marker; cancer therapy;
 KW detection; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 EN WO2002101075-A2.
 XX
 PD 19-DEC-2002.
 XX
 PF 12-JUN-2002; 2002WO-US018638.
 XX
 PR 13-JUN-2001; 2001US-0298155P.
 PR 13-JUN-2001; 2001US-0298159P.
 PR 14-NOV-2001; 2001US-0335936P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
 PI Gannavarapu M, Glatk K, Hoersch S;
 XX
 DR WPI; 2003-156967/15.

DR N-PSDB; ACF12935.
 XX
 PT New isolated nucleic acid molecule useful for detecting, characterizing,
 PT preventing and treating human cervical cancers, in various prognostic and
 PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
 XX
 PS Claim 4; Page 366-367; 386pp; English.
 XX
 CC ACF12928 to ACF12947 encode the human cervical cancer marker proteins (1)
 CC given in ABR92047 to ABR92164. A higher level of expression of (1) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a
 CC vector (II) containing (1); (2) a host cell (III) containing (1); and (3)
 CC assessing (W1) whether a patient is afflicted with cervical cancer,
 CC comprising comparing the level of expression of a marker in a patient's
 CC sample, and the normal level of expression of the marker in a control non
 CC -cervical cancer sample, where a significant increase in the level of
 CC expression of the marker in the patient's sample relative to that in the
 CC control sample is an indication that the patient is afflicted with
 CC cervical cancer. (I) has cytostatic activity, and can be used in gene
 CC therapy and in vaccines. (I) is useful in detecting, characterizing, in
 CC preventing and treating human cervical cancers. (I) may also be used in
 CC various prognostic and diagnostic assays, pharmacogenomics and in
 CC monitoring clinical trials
 XX
 XX Sequence 344 AA;
 CC
 CC Query Match 100.0%; Score 1809; DB 6; Length 344;
 CC Best Local Similarity 100.0%; Pred. No. 8.8e-186;
 CC Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKWMEN 60
 DB 1 MAQKENSYPWPYGRQTAPSGSLTLPQVLRKEPVTSPALVLSRSNVQTPAAPGQKWMEN 60
 QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVH 120
 DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFVNLAREKSHFIVALKVLFKSQIEKEGVH 120
 QY 121 QLRREIEIOAHLHPNHLNLYFYDRIYLLILEYAPRGELYKELQKCTFDEQRTATI 180
 DB 121 QLRREIEIOAHLHPNHLNLYFYDRIYLLILEYAPRGELYKELQKCTFDEQRTATI 180
 QY 181 MEELADALMYCHGKVKVHRDIKPNENLLGLKGLKTIADFGWSVHAPSLRRKTCGTLDY 240
 DB 181 MEELADALMYCHGKVKVHRDIKPNENLLGLKGLKTIADFGWSVHAPSLRRKTCGTLDY 240
 QY 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
 DB 241 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPASVPTGA 300
 QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
 DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQVA 344
 RESULT 8
 ADB80537
 ID ADB80537 standard; protein; 344 AA.
 XX
 AC ADB80537;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Ovarian cancer-associated protein #51.
 XX
 KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
 KW post-operative chemotherapy; radiation therapy; tumour prognosis;
 KW pre-cancerous lesion detection.
 XX
 OS Homo sapiens.
 XX
 PN WO2002102235-A2.
 XX

SQ Sequence 344 AA;

Query Match 100.0%; Score 1809; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 8.8e-186;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTPSALVLSRSNVQPTAAPGQKVMEN 60
 DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTPSALVLSRSNVQPTAAPGQKVMEN 60

QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKFSQIEKEGVEH 120
 DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKFSQIEKEGVEH 120

QY 121 QLRRETEIOAHLHPNLRNYFYDRRIYLIILEYAPRGELYKELQKSTFDEQRTATI 180
 DB 121 QLRRETEIOAHLHPNLRNYFYDRRIYLIILEYAPRGELYKELQKSTFDEQRTATI 180

QY 181 MEELADALMYCHGKVIHRDIKPNELLGLGKELTADFGWSVHAPSLRRKTKWCGTLDYL 240
 DB 181 MEELADALMYCHGKVIHRDIKPNELLGLGKELTADFGWSVHAPSLRRKTKWCGTLDYL 240

QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPPASVPTGA 300
 DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPPASVPTGA 300

QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
 DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 10
 ADN95464
 ID ADN95464 standard; protein; 344 AA.
 AC ADN95464;
 XX ADN95464;

DT 01-JUL-2004 (first entry)
 DE Human BEC/LBC-related protein sequence SeqID387.
 XX growth; differentiation; blood endothelial cell; BEC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGF-3;
 KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
 KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; human.
 XX Homo sapiens.

XX WO2003080640-A1.
 XX 02-OCT-2003.
 XX 07-MAR-2003; 2003WO-US006900.
 XX 07-MAR-2002; 2002US-0363019P.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX (LICN) LICENTIA LTD.
 XX Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
 XX WPI; 2003-876899/81.
 XX N-PSDB; ADN95465.
 XX Example 1; SEQ ID NO 387; 176pp; English.

CC This invention relates to a method of differentially modulating the
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
 CC endothelial cells (LEC) comprises contacting endothelial cells with a
 CC composition comprising an agent that differentially modulates blood or
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
 CC identifying a human subject with lymphoedema and with a mutation in at

CC least one allele of a gene encoding a LEC protein, where the mutation
 CC correlates with lymphoedema in human subjects, and with the proviso that
 CC the LEC protein is not VEGF-3; and administering to the subject a
 CC composition comprising a lymphatic growth agent selected from VEGF-C or
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
 CC the development of compounds with an antiangiogenic, cytostatic,
 CC vasotrophic or antiinflammatory activity or for gene therapy. The method
 CC is useful in modulating the growth or differentiation of blood
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary
 CC lymphoedema, in screening for an endothelial cell disorder or
 CC predisposition to the disorder or in monitoring the efficacy or toxicity
 CC of a drug on endothelial cells. The agent is useful in manufacturing a
 CC medicament for the differential modulation of blood vessel endothelial
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The
 CC lymphatic growth agent may also be used in manufacturing a medicament for
 CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed protein which is related to the method of the invention. Note:
 CC This sequence does not appear in the specification but was obtained by
 CC the indexer using the source data given in table 14 of the specification.

XX Sequence 344 AA;
 SQ Query Match 100.0%; Score 1809; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 8.8e-186;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTPSALVLSRSNVQPTAAPGQKVMEN 60
 DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQVLRKEPVTPSALVLSRSNVQPTAAPGQKVMEN 60

QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKFSQIEKEGVEH 120
 DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKFSQIEKEGVEH 120

QY 121 QLRRETEIOAHLHPNLRNYFYDRRIYLIILEYAPRGELYKELQKSTFDEQRTATI 180
 DB 121 QLRRETEIOAHLHPNLRNYFYDRRIYLIILEYAPRGELYKELQKSTFDEQRTATI 180

QY 181 MEELADALMYCHGKVIHRDIKPNELLGLGKELTADFGWSVHAPSLRRKTKWCGTLDYL 240
 DB 181 MEELADALMYCHGKVIHRDIKPNELLGLGKELTADFGWSVHAPSLRRKTKWCGTLDYL 240

QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPPASVPTGA 300
 DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIYKVDLKFPPASVPTGA 300

QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
 DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344

RESULT 11
 ADK67718
 ID ADK67718 standard; protein; 344 AA.
 AC ADK67718;
 XX ADK67718;

DT 06-MAY-2004 (first entry)
 DE Human modifier of AXIN (MAX) polypeptide.
 XX Human modifier of AXIN; MAX; cytostatic; gene therapy; protein kinase;
 KW enzyme.
 XX Homo sapiens.
 XX WO2004013308-A2.
 XX 12-FEB-2004.

```
PF 06-AUG-2003; 2003WO-US024560.
XX
XX 06-AUG-2002; 2002US-0401534P.
PR 16-SEP-2002; 2002US-0411153P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Gendreau SB, Dora EG, Lickteig K, Amundsen CD;
XX
XX WPI; 2004-157122/15.
DR N-PSDB; ADK67711.
XX
XX Identifying a candidate AXIN pathway-modulating agent, useful in
PT diagnosing and treating cancer, comprises providing an assay system
PT comprising a MAX polypeptide or nucleic acid.
XX
XX Example 1; SEQ ID NO 9; 74pp; English.
XX
XX The present sequence is that of a human modifier of AXIN (MAX)
CC polypeptide characterised as a serine/threonine kinase. Genetic screens
CC were designed to identify modifiers of the axin pathway in Caenorhabditis
CC elegans, where a reduction of function pry-1 (axin) mutant was used.
CC Genes causing altered phenotypes were isolated, and their human
CC homologues, termed MAX, were identified, including the present sequence.
CC These MAX polynucleotides and polypeptides are attractive targets for the
CC treatment of pathologies associated with a defective AXIN signalling
CC pathway, such as cancer. Modulation of MAX or its binding partner is
CC useful for understanding the association of the AXIN pathway and its
CC members in normal and disease conditions and for developing diagnostic
CC and therapeutic modalities for AXIN related pathologies. MAX-modulating
CC agents that act by inhibiting or enhancing MAX expression, directly or
CC indirectly, e.g. by affecting MAX function can be identified using
CC methods of the invention. MAX modulating agents are useful in diagnosis,
CC therapy and pharmaceutical development. Preferred MAX modulating agents
CC include antisense and phosphorothioate morpholino oligomers.
XX
XX SEQ Sequence 344 AA;
Query Match 100.0%; Score 1809; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.8e-186;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
QY 121 QLRRETEIOAHLHPNLRILYNYFYDRRRILYLLIYAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETEIOAHLHPNLRILYNYFYDRRRILYLLIYAPRGELYKELQKCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVIHRDIPENLLGLKGLKIADFGWSVHAPSLRRKTKWCGTLDYL 240
DB 181 MEELADALMYCHGKKVIHRDIPENLLGLKGLKIADFGWSVHAPSLRRKTKWCGTLDYL 240
QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
RESULT 12
ADQ89834
ID ADQ89834 standard; protein; 344 AA.
XX
XX ADQ89834;
XX
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```
DT 21-OCT-2004 (first entry)
XX
XX Antagonist of cell cycle progression polypeptide #132.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
XX Homo sapiens.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Glover D, Bell G, Frenz L, Midgley C;
XX
XX WPI; 2004-544089/52.
DR N-PSDB; ADQ89833.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 264; 461pp; English.
XX
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
XX SEQ Sequence 344 AA;
Query Match 100.0%; Score 1809; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.8e-186;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
DB 1 MAQKENSYPWPYGRQTAPSGSLTPQVLRKEPVPSPALVMSRSNVQPTAAPGQKVMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSQIEKEGVEH 120
QY 121 QLRRETEIOAHLHPNLRILYNYFYDRRRILYLLIYAPRGELYKELQKCTFDEQRTATI 180
DB 121 QLRRETEIOAHLHPNLRILYNYFYDRRRILYLLIYAPRGELYKELQKCTFDEQRTATI 180
QY 181 MEELADALMYCHGKKVIHRDIPENLLGLKGLKIADFGWSVHAPSLRRKTKWCGTLDYL 240
DB 181 MEELADALMYCHGKKVIHRDIPENLLGLKGLKIADFGWSVHAPSLRRKTKWCGTLDYL 240
QY 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
DB 241 PPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPSASHNETYRRIYKVDLKFPSVPTGA 300
QY 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
DB 301 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV 344
```


RESULT 13
ABM81826
ID ABM81826 standard; protein; 344 AA.
XX
AC ABM81826;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO70812, SEQ:4700.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN40117.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 4700; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 1809; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.8e-186;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAQKENSYPWPGYGRQTAPSGLSLTPQVLRKEPVTSPSALVMSRSNVQPTAAPGQKWMEN 60
|||||

Db 1 MAQKENSYPWPGYGRQTAPSGLSLTPQVLRKEPVTSPSALVMSRSNVQPTAAPGQKWMEN 60
QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYAREKKSHFIVALKVLFKSQIEKEGVEH 120
|||
Db 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYAREKKSHFIVALKVLFKSQIEKEGVEH 120
|||
QY 121 OLREIEIQAHLLHHPNLTLYNYFYDRRRRIYLYLEVAPRGELYKELQKSCCTFEQRTATI 180
|||
Db 121 OLREIEIQAHLLHHPNLTLYNYFYDRRRRIYLYLEVAPRGELYKELQKSCCTFEQRTATI 180
|||
QY 181 MEELADALMYCHGKVKVHRDIKDPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTLDYL 240
|||
Db 181 MEELADALMYCHGKVKVHRDIKDPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTLDYL 240
|||
QY 241 PPMIEGRMNEKVDLWCIGLVLCYELLVGNPPFESASHNETYRRIKVDLKFASVPTGA 300
|||
Db 241 PPMIEGRMNEKVDLWCIGLVLCYELLVGNPPFESASHNETYRRIKVDLKFASVPTGA 300
|||
QY 301 QDLISKLLRHNPSERLPLAQVSAHPVWANSRRLVPPSALQSV 344
|||
Db 301 QDLISKLLRHNPSERLPLAQVSAHPVWANSRRLVPPSALQSV 344
|||

RESULT 14

ABR61580
ID ABR61580 standard; protein; 344 AA.
XX

AC ABR61580;
XX

DT 15-JAN-2004 (first entry)
XX

DE Human HsAIRK-2 (Aurora A) protein.
XX

KW RasGAP; Aurora kinase; cytostatic; anti-tumoural; human; HsAIRK-2;
KW Aurora A.
XX

OS Homo sapiens.
XX

PN WO2003087395-A2.
XX

PD 23-OCT-2003.
XX

PF 15-APR-2003; 2003WO-IB002972.
XX

PR 15-APR-2002; 2002US-0372483P.
XX

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX

PI Garbay C, Gigoux V, Camonis J, L'hoste S, Samson J;
XX

WPI; 2003-845340/78.
DR

N-PSDB; ACF58069.
XX

PT Identifying anti-tumoral compounds, comprises determining the capacity of
PT a compound to inhibit interaction between RasGAP and Drosophila
PT melanogaster (Dm) aurora kinase, or between RasGAP, Dm aurora kinase and
PT aurora binding protein.
XX

PS Disclosure; Page 62-63; Opp; English.
XX

CC The invention relates to identifying a biologically active compound with
CC anti-tumoral properties, where the compound is studied for its capacity
CC to inhibit the interaction between* (a) RasGAP and the Drosophila
CC melanogaster Aurora kinase or an orthologue of the kinase, or its
CC fragment able to interact with RasGAP; or (b) RasGAP, an Aurora-binding
CC protein and the D. melanogaster Aurora kinase or an orthologue of the
CC kinase, or its fragment. The method is useful for identifying anti-
CC tumoral agents. The present sequence represents a human HsAIRK-2 (Aurora
CC A) protein, an orthologue of the D. melanogaster Aurora kinase
XX
SQ Sequence 344 AA;

Query Match 99.7%; Score 1803; DB 7; Length 344;

Best Local Similarity 99.7%; Pred. No. 3.9e-185;		Matches 343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MAOKENSYPWPGYGRQTAPSGSLTLPQRLKKEPVTSPALVMSRSNVQPTAAPGQKVMEN	60
Db	1	MAOKENSYPWPGYGRQTAPSGSLTLPQRLKKEPVTSPALVMSRSNVQPTAAPGQKVMEN	60
QY	61	SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKEGVH	120
Db	61	SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKEGVH	120
QY	121	QLRRETEIQAHLHHPNLRNYFYDRRIYLIILEYAPRGELYKELQKCTFDEQRTAT	180
Db	121	QLRRETEIQAHLHHPNLRNYFYDRRIYLIILEYAPRGELYKELQKCTFDEQRTAT	180
QY	181	MEELADALMYCHGKVKVTHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCGTL	240
Db	181	MEELADALMYCHGKVKVTHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCGTL	240
QY	241	PPMEMIEGRMNEKVDLWCIGVLCYELLVGNPPPFESASHNETYRRIYVKVDLKFPASVPTGA	300
Db	241	PPMEMIEGRMNEKVDLWCIGVLCYELLVGNPPPFESASHNETYRRIYVKVDLKFPASVPTGA	300
QY	301	QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV	344
Db	301	QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV	344
RESULT 15			
AAV27052	ID	AAV27052 standard; protein; 347 AA.	
AC	AAV27052;		
XX	08-OCT-1999	(first entry)	
DE	Human protein kinase (HPKM)-1 (clone ID 2940).		
XX	Human protein kinase molecule; HPKM; human; protein kinase;		
XX	phosphate group; cancer; immune disorder.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	60	Modified-site	/note= "potential N-glycosylation site"
FT	73	Modified-site	/note= "potential phosphorylation site"
FT	83..106	Domain	/note= "potential signature sequence for protein kinase catalytic domain"
FT	111	Modified-site	/note= "potential phosphorylation site"
FT	171	Modified-site	/note= "potential phosphorylation site"
FT	179	Modified-site	/note= "potential phosphorylation site"
FT	199..211	Domain	/note= "potential signature sequence for protein kinase catalytic domain"
FT	230	Modified-site	/note= "potential phosphorylation site"
FT	235	Modified-site	/note= "potential phosphorylation site"
FT	280	Modified-site	/note= "potential phosphorylation site"
FT	282	Modified-site	/note= "potential N-glycosylation site"
FT	284	Modified-site	/note= "potential phosphorylation site"
FT	316	Modified-site	/note= "potential phosphorylation site"
FT	334	Modified-site	/note= "potential phosphorylation site"
/note= "potential phosphorylation site"			
FT	PN	WO9938981-A2.	
XX	05-AUG-1999.		
XX	12-JAN-1999;	99WO-US000661.	
XX	30-JAN-1998;	98US-00016000.	
XX	(INCY-) INCYTE PHARM INC.		
XX	Bandman O, Hillman JL, Lal P, Akerblom IE, Shah P, Corley NC;		
XX	Guegler KJ;		
XX	WPI; 1999-479190/40.		
XX	N-PSDB; AAX89850.		
XX	New human protein kinase molecules useful for treating or preventing cancer or an immune disorder.		
XX	Claim 1; Page 64-65; 77pp; English.		
XX	The invention provides human protein kinase molecules (HPKM) (AAV27052-57) and nucleic acid sequences (AAX89850-55) encoding the HPKM polypeptides respectively. The HPKM polypeptides can be produced recombinantly by standard recombinant methodology. Protein kinases add phosphate groups to proteins. HPKM polypeptide or an HPKM antagonist is used to treat or prevent cancer or an immune disorder. The present sequence represents the amino acid sequence of HPKM-1		
XX	Sequence 347 AA;		
Query Match 99.4%; Score 1797.5; DB 2; Length 347;			
Best Local Similarity 99.1%; Pred. No. 1.6e-184;			
Matches 344; Conservative 0; Mismatches 0; Indels 3; Gaps 1;			
QY	1	MAOKENSYPWPGYGRQTAPSGSLTLPQRLKKEPVTSPALVMSRSNVQPTAAPGQKVMEN	60
Db	1	MAOKENSYPWPGYGRQTAPSGSLTLPQRLKKEPVTSPALVMSRSNVQPTAAPGQKVMEN	60
QY	61	SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKEGVH	120
Db	61	SSGTPDILTRHFTIDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLPKFSQIEKEGVH	120
QY	121	QLRRETEIQAHLHHPNLRNYFYDRRIYLIILEYAPRGELYKELQKCTFDEQRTAT	179
Db	121	QLRRETEIQAHLHHPNLRNYFYDRRIYLIILEYAPRGELYKELQKCTFDEQRTAT	180
QY	180	--IMEELADALMYCHGKVKVTHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCGTL	237
Db	181	RAIMEELADALMYCHGKVKVTHRDIKPENLLGLKGLKIADFGWSVHAPSLRRKTCGTL	240
QY	238	DYLPPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPFESASHNETYRRIYVKVDLKFPASVP	297
Db	241	DYLPPEMIEGRMNEKVDLWCIGVLCYELLVGNPPPFESASHNETYRRIYVKVDLKFPASVP	300
QY	298	TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV	344
Db	301	TGAQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPSPALQSV	347
RESULT 16			
ABU57643	ID	ABU57643 standard; protein; 347 AA.	
XX	AC	ABU57643;	
XX	09-APR-2003	(first entry)	
XX	Differentially expressed breast cancer associated protein #30.		
XX	Breast cancer; differential gene expression; BC-cDNA;		

KW breast cancer diagnosis; breast cancer monitoring;
XX breast cancer treatment; breast cancer staging.

XX Homo sapiens.

XX US2002156263-A1.

XX 24-OCT-2002.

XX 04-OCT-2001; 2001US-00974298.

XX 05-OCT-2000; 2000US-0238331P.

XX (CHEN/) CHEN H.

XX Chen H;

XX WPI; 2003-182653/18.

XX New cDNAs, which are differentially expressed in (metastatic) breast
PT cancer useful for diagnosing or staging, breast cancer, or for monitoring
PT the treatment of breast cancer in an individual.

XX Example; SEQ ID NO 136; 30pp; English.

XX The invention describes a combination of cDNAs (designated BC-cDNAs),
CC which are differentially expressed in breast cancer. The combination
CC includes 152 cDNA sequences, or their complements. The protein encoded by
CC any of these BC-cDNAs is useful for screening several molecules or
CC compounds to identify at least one ligand that specifically binds the
CC protein, producing or preparing polyclonal or monoclonal antibodies, or
CC purifying antibodies from a sample. The antibodies, which specifically
CC bind the protein differentially expressed in breast cancer is useful for
CC detecting the expression of a protein in a sample. The BC-cDNAs are also
CC useful for diagnosing, monitoring the treatment of, or staging, breast
CC cancer. This is the amino acid sequence of a differentially expressed
CC breast cancer associated protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=20020156263

XX Sequence 347 AA;

Query Match 99.4%; Score 1797.5; DB 6; Length 347;
Best Local Similarity 99.1%; Pred. No. 1.6e-184;
Matches 344; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQRLKKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60

DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQRLKKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60

QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSOIEKEGVEH 120

DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSOIEKEGVEH 120

QY 121 QLRRETEIOAHLHPNLRNLYNYFYDRRRYLYILEYAPRGELYKELQKCTFDEQRTAT- 179

DB 121 QLRRETEIOAHLHPNLRNLYNYFYDRRRYLYILEYAPRGELYKELQKCTFDEQRTATV 180

QY 180 --IMEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTL 237

DB 181 RAIMELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTL 240

QY 238 DYLPPEMIEGRMNEKVDLWCIGVLYELVGNPPPSASHNETHYRRIYKVDLKFPPASVP 297

DB 241 DYLPPEMIEGRMNEKVDLWCIGVLYELVGNPPPSASHNETHYRRIYKVDLKFPPASVP 300

QY 298 TGAQDLISKLLRNPNSERLPLAQVSAHPWPVANSRRVLPESALQSWA 344

DB 301 TGAQDLISKLLRNPNSERLPLAQVSAHPWPVANSRRVLPESALQSWA 347

RESULT 17

ADM72221
ID ADM72221 standard; protein; 343 AA.

XX AC ADM72221;

XX DT 17-JUN-2004 (first entry)

XX DE Human TASK112 polypeptide.

XX KW TASK; tumour-associated kinase; cytostatic; tumour antigen;
cell proliferative disorder; cancer; transgenic; human.

XX OS Homo sapiens.

XX PN WO2004024064-A2.

XX PD 25-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027894.

XX PR 11-SEP-2002; 2002US-0410166P.

XX PA (GETH) GENENTECH INC.

XX PI Desauvage EV, Wood WI, Zhang Z;

XX DR WPI; 2004-282985/26.

XX DR N-PSDB; ADM72220.

XX PT New tumor-associated kinase nucleic acids and polypeptides, useful as
hybridization probes for isolating full length TASK DNA, for generating
transgenic animals, in chromosome identification, or for tissue typing.
XX Claim 12; SEQ ID NO 26; 163pp; English.

XX The invention relates to new isolated tumour-associated kinase (TASK)
nucleic acid molecules and encoded polypeptides. Cytostatic. The
antibody, oligopeptide or organic molecule that binds to the TASK
polypeptide are useful for treating a mammal having a tumour comprising
cells expressing the polypeptide. Antagonists of TASK are useful for
treating or preventing a cell proliferative disorder (e.g. cancer)
associated with increased expression or activity of TASK polypeptide. The
TASK polynucleotides and polypeptides may be used as hybridization probes
for isolating full length TASK DNA, for generating transgenic animals, in
chromosome identification, or for tissue typing. The present sequence
represents a human TASK polypeptide.

XX Sequence 343 AA;

Query Match 97.9%; Score 1770.5; DB 8; Length 343;
Best Local Similarity 98.8%; Pred. No. 1.3e-181;
Matches 340; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MAQKENSYPWPGYGRQTAPSGSLTPQRLKKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60

DB 1 MAQKENSYPWPGYGRQTAPSGSLTPQRLKKEPVTSPALVLSRSNVQPTAAPGQKVMEN 60

QY 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSOIEKEGVEH 120

DB 61 SSGTDPILTRHFTIDDFEIGRPLGKGFNGVYLAREKKSHFIVALKVLFKSOIEKEGVEH 120

QY 121 QLRRETEIOAHLHPNLRNLYNYFYDRRRYLYILEYAPRGELYKELQKCTFDEQRTATI 180

DB 121 QLRRETEIOAHLHPNLRNLYNYFYDRRRYLYILEYAPRGELYKELQKCTFDEQRTATI 180

QY 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTL 240

DB 181 MEELADALMYCHGKKVIHRDIKPENLLGLKGLKIADFGWSVHAPSLRRTKTCGTL 240

QY 241 PEMIEGRMNEKVDLWCIGVLYELVGNPPPSASHNETHYRRIYKVDLKFPPASVPTGA 300

DB 241 PEMIEGRMNEKVDLWCIGVLYELVGNPPPSASHNETHYRRIYKVDLKFPPASVPTGA 299


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PR 29-MAR-2002; 2002US-0368760P.
XX (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
XX
PI Hopkins N, Golling G, Amsterdam A, Sun Z;
XX
XX WPI; 2004-304692/28.
DR N-PSDB; ADO57330.
XX
XX New 459 nucleic acids and encoded polypeptides, useful for diagnosing,
PT treating or preventing a kidney disorder in an organism, or in screening
PT for compounds that modulate the development of an organism.
XX
XX Disclosure; SEQ ID NO 98; 347pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) comprising
CC a sequence having at least 75% sequence identity to the 459 nucleic acid
CC sequence of 2808 base pairs (SEQ ID NO: 59) given in the specification,
CC over at least 600 contiguous base pairs, where the nucleic acid functions
CC in kidney development. (I) is useful for treating or preventing a kidney
CC disorder in an organism, where the nucleic acid elicits an alteration in
CC expression of a 459 nucleic acid sequence in the organism and
CC subsequently treats or prevents a kidney disorder. The nucleic acid may
CC also be used in diagnosing, preventing and treating a variety of
CC mammalian diseases and developmental disorders (e.g. circulatory
CC disorders, hearing disorders, heart defect, infertility, stroke, mental
CC retardation, muscle defects, proliferative disorders, or bone defects or
CC disorders) as well as in screening for compounds that modulate the
CC development of an organism as a whole or of specific tissues or organs
CC within that organism. This is the amino acid sequence of a kidney
CC development associated protein.
XX
XX Sequence 320 AA;
SQ
Query Match 62.1%; Score 1124; DB 8; Length 320;
Best Local Similarity 65.7%; Pred. No. 6.2e-112;
Matches 224; Conservative 33; Mismatches 52; Indels 32; Gaps 4;
QY 1 MAOKENSYWPYGRQTAPSGSLTPQRLVRKEPVTPTSAVLMSRSNVQP---TAAPGQK 56
DB 1 MQNKENREP-----RVQQ-----TPSAGVGPLRVENPDPHTHAVSGGRV 39
QY 57 VMENSGTPTDILTRHFTIDDFEIGRPLGKGFNGVILAREKKSHFIVALKVLFKSTQKE 116
DB 40 PVKSNS-----KVLSDIDDFDGRPLGKGFNGVILAREKKLVVIALKLVFKSQMVK 92
QY 117 GVVEHQLRRETEIQAHLLHPNLRILNYFYDORRRIYLIYAPRGELYKELQKSTFDEQR 176
DB 93 GVVEHQLRRETEIQSHLRHPNLRPNYFHDTRVFLILEYAPRGEMYKELQRYGHFDQDQ 152
QY 177 TATIMEELADALMYCHCKKVIHRDIDKENLLGLKGELKTADFQWSVHAPSLARKTCMGT 236
DB 153 TATIMEVSDALQVCHCKKVIHRDIDKENLLGLGKELKTADFQWSVHAPSLARRTCMGT 212
QY 237 LDYLPPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPESPESASHNETVRRIVKVLKFPASV 296
DB 213 LDYLPPEMIEGSHDEKVDLWSIGVLCYECVLGNPPETPETHQAEYKRIKVDLPFKLV 272
QY 297 PTGAQDLISKLLRHNSERPLAQVSNHPWVRNSRVLPP 337
DB 273 SEGARDLISKLLRHSPMRPLPLRSVMHGRGVKANSRVLPP 313
RESULT 25
AAW18084
ID AAW18084 standard; protein; 403 AA.
XX
AC AAW18084;
XX
DT 07-SEP-1997 (first entry)

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XX DE Human Aurora-2.
XX KW Aurora-2; AUR-2; signal transduction; protein kinase; tumour; cancer;
XX KW protein kinase; gene therapy; diagnosis; antibody.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..130
XX /label= N-terminal_domain
XX Misc-difference 50
XX /note= "deduced residue from some cDNA clones is Leu"
XX Misc-difference 50
XX /note= "deduced residue from some cDNA clones is Leu"
XX Misc-difference 57
XX /note= "deduced residue from some cDNA clones is Ile"
XX Misc-difference 57
XX /note= "deduced residue from some cDNA clones is Ile"
XX Domain 131..403
XX /label= Kinase_domain
XX Modified-site 288
XX /label= Phosphorylation
XX /note= "cAMP-dependent protein kinase phosphorylation
XX site conserved in AUR-2 and yeast and Drosophila
XX homologues"
XX Modified-site 334
XX /label= Phosphorylation
XX /note= "tyrosine phosphorylation consensus site conserved
XX in Drosophila aurora but not in AUR-1 or yeast IPL1"
XX Modified-site 342
XX /label= Phosphorylation
XX /note= "cAMP-dependent protein kinase phosphorylation
XX site conserved in AUR-2 and yeast and Drosophila
XX homologues"
XX
XX WO9722702-A1.
XX
XX 26-JUN-1997.
XX
XX 25-NOV-1996; 96WO-US018859.
XX
XX 18-DEC-1995; 95US-0008809P.
XX 14-AUG-1996; 96US-0023943P.
XX
XX (SUGB-) SUGEN INC.
XX
XX Plowman GD, Mossie KG;
XX
XX WPI; 1997-341693/31.
XX N-PSDB; AAT67290.
XX
XX Aurora-1 and Aurora-2 and related genes - useful in tumour gene therapy.
XX Claim 3; Page 83-85; 98pp; English.
XX
XX Novel human proteins, termed Aurora-1 (AAW18083) and Aurora-2 (AAW18084)
XX (AUR-1 and AUR-2), are related serine/threonine kinases with short N-
XX terminal extensions that appear to be involved in cancer and/or signal
XX transduction disorders. Their amino acid sequences were deduced from to
XX pancreatic tumour cDNA clones (AAT67289-90). AUR-1 and AUR-2 appear to
XX regulate nuclear division, with disruption of their signaling resulting
XX in polyploid cells. AUR-2 RNA is low or absent in most normal tissues,
XX and abundant in a subset of tumour-derived cell lines, partic. those of
XX colorectal origin. AUR polypeptides can be expressed in host cells and
XX used to raise diagnostic antibodies and to screen for compounds that
XX interact with AUR-1 and/or AUR-2
XX
XX Sequence 403 AA;
Query Match 58.5%; Score 1057.5; DB 2; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

```


XX The specification describes human protein kinase/protein phosphatases. It
 CC is expected that the protein kinase/protein phosphatase gene participates
 CC in signal transduction in cells. The protein kinase/protein phosphatase
 CC polypeptides and polynucleotides are useful for developing diagnostics
 CC and treatment agents for human and animal diseases. The protein
 CC kinase/protein phosphatase polypeptides are useful as target molecules in
 CC designing novel drugs. The protein kinase/protein phosphatase
 CC polynucleotides are useful as a source of probes and primers, which may
 CC be used to isolate homologous sequences. The present sequence represents
 CC a human protein, which is used in the course of the invention
 XX
 SQ Sequence 403 AA;

Query Match 58.5%; Score 1057.5; DB 4; Length 403;
 Best Local Similarity 63.2%; Pred. No. 1.3e-104;
 Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQPVLR-----KEPVTSALVMSRSNVQPTAAPGQKWMENSSGTPDILTRHFT 73
 DB 82 TSPVHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKQTEKEGVHQLRRETEIOAHLH 133
 DB 130 LEDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKQTEKEGVHQLRRETEIOAHLH 189

QY 134 HPNILRLNYFYDRIIRYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193
 DB 190 HPNILRLNYFYDRIIRYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 249

QY 194 KVIHREDIKPENLLGLKGLKADFGVSHVAPSLRKTKMCGTLDYLPPEMIEGRMNEK 253
 DB 250 KVIHREDIKPENLLGLKGLKADFGVSHVAPSLRKTKMCGTLDYLPPEMIEGRMNEK 309

QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLRLHNS 313
 DB 310 VDLWISGLVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLRLHNS 369

QY 314 ERLPLAQVSAHPVWVRANSRRLVPPSALQS 342
 DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 28
 AAG67435
 ID AAG67435 standard; protein; 403 AA.
 AC AAG67435;
 XX
 XX 26-NOV-2001 (first entry)
 XX Amino acid sequence of a human polypeptide.
 XX
 DE Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 XX
 OS Homo sapiens.
 XX WO200109345-A1.
 XX
 XX 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-JP005060.
 XX
 XX 29-JUL-1999; 99JP-00248036.
 PR 18-OCT-1999; 99US-0159590P.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 17-FEB-2000; 2000US-0183322P.
 PR 02-MAY-2000; 2000JP-00183767.
 XX
 XX (HELI-) HELIX RES INST.
 PA
 XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 PI

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
 PI Senoo C, Nezu J;
 XX
 DR WPI; 2001-564736/63.
 XX
 PT New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes.
 XX
 PS Example 4; Page 196-199; 336pp; Japanese.
 XX
 CC The specification describes human protein kinase/protein phosphatases.
 CC The polypeptides are expected to participate in signal transduction in
 CC cells. The kinase phosphatases are connected with intracellular
 CC signalling pathways. Antisense oligonucleotides and compounds identified
 CC by screening (agonists or antagonists) can be used to treat human or
 CC animal disorders associated with the expression or function of the
 CC protein. In addition, the polypeptides may be used as target molecules
 CC for drug development. The present sequence represents a polypeptide, used
 CC in the course of the invention
 XX
 SQ Sequence 403 AA;

Query Match 58.5%; Score 1057.5; DB 4; Length 403;
 Best Local Similarity 63.2%; Pred. No. 1.3e-104;
 Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQPVLR-----KEPVTSALVMSRSNVQPTAAPGQKWMENSSGTPDILTRHFT 73
 DB 82 TSPVHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKQTEKEGVHQLRRETEIOAHLH 133
 DB 130 LEDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKQTEKEGVHQLRRETEIOAHLH 189

QY 134 HPNILRLNYFYDRIIRYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 193
 DB 190 HPNILRLNYFYDRIIRYILLEYAPRGELYKELQKCTFDEQRTATIMEELADALMYCHG 249

QY 194 KVIHREDIKPENLLGLKGLKADFGVSHVAPSLRKTKMCGTLDYLPPEMIEGRMNEK 253
 DB 250 KVIHREDIKPENLLGLKGLKADFGVSHVAPSLRKTKMCGTLDYLPPEMIEGRMNEK 309

QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLRLHNS 313
 DB 310 VDLWISGLVLCYELLVGNPPFESASHNETYRRIVKVDLKPASVPTGAQDLISKLRLHNS 369

QY 314 ERLPLAQVSAHPVWVRANSRRLVPPSALQS 342
 DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 29
 ABP97367
 ID ABP97367 standard; protein; 403 AA.
 XX
 AC ABP97367;
 XX
 XX 10-MAY-2003 (first entry)
 XX
 DE Human serine/threonine kinase 15 (STK15), Ile31 variant.
 XX
 KW Human; serine/threonine kinase 15; STK15; STK6; Aurora2; cell cycle;
 KW chromosome 20; centrosome-associated kinase; cancer susceptibility;
 KW single nucleotide polymorphism; SNP; genetic diagnosis; prognosis;
 KW detection; diagnosis; cancer; malignant astrocytoma; glioblastoma;
 KW medulloblastoma; gastric cancer; colorectal cancer; colorectal adenoma;
 KW acute myelogenous leukaemia; lung cancer; renal cancer; leukaemia;
 KW breast cancer; prostate cancer; endometrial cancer; neuroblastoma;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX

PR 15-APR-2002; 2002US-00123731.
PR 16-APR-2002; 2002US-0373366P.
PA (RIGB-) RIGEL PHARM INC.
XX Hitoshi Y, Jenkins Y;
XX WPI; 2003-865396/80.
DR N-PSDB; ADF61839.
XX Identifying a compound that modulates cell cycle arrest, for treating
PT e.g. cancer, comprises contacting a cell comprising a target polypeptide
PT and determining the chemical or phenotypic effect of the compound upon
PT the cell.
XX Claim 1; SEQ ID NO 24; 176pp; English.
PS The invention relates to a novel method for identifying a compound that
XX modulates cell cycle arrest comprising contacting a target polypeptide
CC within a cell with a compound and determining the chemical or phenotypic
CC effect of the compound upon the cell. The method of the invention has
CC cytostatic, antiproliferative, antiarteriosclerotic, vasotropic and
CC antithyroid applications and may be useful for identifying a compound
CC that modulates cell cycle arrest. Such compounds may subsequently be used
CC for developing therapeutic reagents to treat melanoma, breast, ovarian,
CC lung, gastrointestinal or colon cancer, as well as other proliferative
CC diseases such as Grave's disease, psoriasis, atherosclerosis, restenosis
CC and other vasoproliferative diseases. The current sequence is that of the
CC human serine/threonine kinase 15 (STK15/ARK2) protein of the invention.
XX Sequence 403 AA;
SQ Query Match 58.5%; Score 1057.5; DB 7; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104; Indels 23; Gaps 5;
Matches 208; Conservative 41; Mismatches 57;
QY 22 STLQPVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMNSGTPDILTRHFT 73
DB 82 TSVPHVPSRPLNNTQSKQPL-PSA----PENNPEELASKQKVESKK-----RQWA 129
QY 74 IDDFEIGRLGKGFNVILARBKSHFIVALKVLPKSLQIEKGVHQLAREIEIOAHLH 133
DB 130 LEDFEIGRLGKGFNVILAREKQKFLALKVPKQLEKAGVHEQLRREVEIQSHLR 189
QY 134 HPNILRLYNYFDRRIYLLILEVAPRGELYKELQKCTDEORTATIMEELADALMVCHG 193
DB 190 HPNILRLYGYFHDTATVYLLILEVAPRGELYKELQKCTDEORTATIMEELADALMVCHG 249
QY 194 KVIHRDIPENLLGLKGLKELADFGWSVHAPSLRRKTCMGTLDYLPPEMIEGRMHNEK 253
DB 250 KVIHRDIPENLLGSAGELKADFGWSVHAPSLRRRTILCGTLDYLPPEMIEGRMHDEK 309
QY 254 VDLWCTGVLCYELLGNPPESHNETVRIYVKVLDLKPASVPTGAQDLISKLRLHNS 313
DB 310 VDLWSLGVLCYELGVGKPPPEANTYQETVKRISRVFTDFVTEGARDLISRLKHNS 369
QY 314 ERLPLQVSAHPMVANSRVLPSALQS 342
DB 370 QRPMLREVLHPMITANSSK---PSNCQN 395
RESULT 33
ADN3988
ID ADN3988 standard; protein; 403 AA.
XX ADN3988;
XX AC
XX AC
DT 17-JUN-2004 (first entry)
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C258.
DE Human; differential expression; cancer; angiogenic disorder;
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX Homo sapiens.
OS WO2003042661-A2.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-US036810.
XX PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA Afar D, Ariz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR N-PSDB; ADN39671.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX Claim 12; SEQ ID NO C258; 1385pp; English.
XX The invention relates to nucleic acids and proteins (ADN39683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX Sequence 403 AA;
SQ Query Match 58.5%; Score 1057.5; DB 7; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLQPVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMNSGTPDILTRHFT 73
DB 82 TSVPHVPSRPLNNTQSKQPL-PSA----PENNPEELASKQKVESKK-----RQWA 129
QY 74 IDDFEIGRLGKGFNVILARBKSHFIVALKVLPKSLQIEKGVHQLAREIEIOAHLH 133
DB 130 LEDFEIGRLGKGFNVILAREKQKFLALKVPKQLEKAGVHEQLRREVEIQSHLR 189
QY 134 HPNILRLYNYFDRRIYLLILEVAPRGELYKELQKCTDEORTATIMEELADALMVCHG 193
DB 190 HPNILRLYGYFHDTATVYLLILEVAPRGELYKELQKCTDEORTATIMEELADALMVCHG 249
QY 194 KVIHRDIPENLLGLKGLKELADFGWSVHAPSLRRKTCMGTLDYLPPEMIEGRMHNEK 253
DB 250 KVIHRDIPENLLGSAGELKADFGWSVHAPSLRRRTILCGTLDYLPPEMIEGRMHDEK 309
QY 254 VDLWCTGVLCYELLGNPPESHNETVRIYVKVLDLKPASVPTGAQDLISKLRLHNS 313
DB 310 VDLWSLGVLCYELGVGKPPPEANTYQETVKRISRVFTDFVTEGARDLISRLKHNS 369
QY 314 ERLPLQVSAHPMVANSRVLPSALQS 342
DB 370 QRPMLREVLHPMITANSSK---PSNCQN 395
RESULT 33
ADN3988
ID ADN3988 standard; protein; 403 AA.
XX ADN3988;
XX AC
XX AC
DT 17-JUN-2004 (first entry)
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C258.
DE Human; differential expression; cancer; angiogenic disorder;
XX fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

Db 82 TSPHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNEESKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQRLAREIEIOAHLH 133
Db 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKLVFKAQLEKAGVEHQRLAREIEIOAHLH 189
QY 134 HPNILRLYNYFYDRIIRYILILEYAPRGELYKELQKCTFDEORTATIMEELADALMYCHG 193
Db 190 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATITELANALSYCHS 249
QY 194 KKVIRHDIKPENLILGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
Db 250 KKVIRHDIKPENLILGLSAGELKIADFGWSVHAPSSRRTILCGTLDYLPPEMIEGRMHDEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVVKDLKFPASVPTGAQDLISKLLRHNP 313
Db 310 VDLWSLGVLCYELFVGKPPFEANTYQETVKRISRVEFTFPDFVTEGARDLISRLKHNP 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 34
ADE15337
ID ADE15337 standard; protein; 403 AA.
XX AC ADE15337;
XX
DT 29-JAN-2004 (first entry)
XX
DE Truncated Aurora-2 kinase #SEQ ID 1.
XX
KW Aurora-2 kinase; three dimensional structure; protein co-ordinate data.
XX
OS Homo sapiens.
XX
PN WO2003092607-A2.
XX
PD 13-NOV-2003.
XX
PF 01-MAY-2003; 2003WO-US013605.
XX
PR 01-MAY-2002; 2002US-0377510P.
XX
PA (VERT-) VERTEX PHARM INC.
XX
PI Cheatham G, Knegetel R, Swenson L, Coll JT, Renwick S, Weber P;
XX
PS WPI; 2004-022617/02.
XX
PT Crystal useful for screening, designing and evaluating compounds as
PT agonists or antagonists of Aurora-2 kinases, comprises optionally
PT phosphorylated Aurora-2 kinase domain.
XX
PS Example 1; SEQ ID NO 1; 242pp; English.
XX
CC The invention relates to a crystal comprising an optionally
CC phosphorylated Aurora-2 kinase domain or its homologue. The protein of
CC the invention may be used for identifying agonists or antagonists of
CC Aurora-2 kinases, and for generation of three dimensional structures and
CC structural co-ordinate information of Aurora family proteins. The
CC crystalline structure facilitates the designing of selective inhibitors
CC of Aurora family kinases (particularly Aurora-2 kinase) so that
CC undesirable side effects associated with non-selective inhibitors can be
CC avoided. The structural co-ordinates solve the structure of Aurora-2
CC proteins that have amino acid substitutions, additions and/or mutations,
CC and serve as additional tools to determine the most efficient binding
CC interactions. The current sequence represents the Aurora-2 kinase amino
CC acid sequence.
XX
SQ Sequence 403 AA;

Query Match 58.5%; Score 1057.5; DB 8; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLPOQVLR-----KEPVTPSALVLSMSRSNVQPTAAPGQKVMENSSGTPDILTRHFT 73
Db 82 TSPHPVSRPLNNTQKSKQPL-PSA-----PENNPEELASKQKNEESKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFIVALKVLFKSOIEKEGVHQRLAREIEIOAHLH 133
Db 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKLVFKAQLEKAGVEHQRLAREIEIOAHLH 189
QY 134 HPNILRLYNYFYDRIIRYILILEYAPRGELYKELQKCTFDEORTATIMEELADALMYCHG 193
Db 190 HPNILRLYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEORTATITELANALSYCHS 249
QY 194 KKVIRHDIKPENLILGLKGLKGIADFGWSVHAPSLRRKTKMCGTLDYLPPEMIEGRMHNEK 253
Db 250 KKVIRHDIKPENLILGLSAGELKIADFGWSVHAPSSRRTILCGTLDYLPPEMIEGRMHDEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRVVKDLKFPASVPTGAQDLISKLLRHNP 313
Db 310 VDLWSLGVLCYELFVGKPPFEANTYQETVKRISRVEFTFPDFVTEGARDLISRLKHNP 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
Db 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 35
ADH59556
ID ADH59556 standard; protein; 403 AA.
XX AC ADH59556;
XX
DT 25-MAR-2004 (first entry)
XX
DE Monoclonal antibody of the invention.
XX
KW Monoclonal antibody; Mab; aurora-A kinase; Cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003106500-A1.
XX
PD 24-DEC-2003.
XX
PF 12-JUN-2003; 2003WO-FR001772.
XX
PR 12-JUN-2002; 2002FR-00007212.
XX
PA (CNRS) CENT NAT RECH SCI.
PA (FRSA-) ETAB FR DU SANG-BRETAGNE.
XX
PI Prigent C, Martin A;
XX
DR WPI; 2004-071550/07.
DR N-PSDB; ADH59555.
XX
PT New monoclonal antibody specific for aurora-A kinase, useful for
PT diagnosis, prognosis and treatment of solid tumors, also for drug
PT screening.
XX
PS Claim 8; SEQ ID NO 2; 38pp; French.
XX
CC The present invention relates to monoclonal antibody (MAB) that
CC recognizes specifically the human or murine aurora-A kinase binds to
CC membranes that contain, can detect and optionally purify by
CC immunoprecipitation, stains biological tissues where is secreted and does
CC not inhibit the enzymatic activity of MAB. Cytostatic. MAB are used for
CC in vitro diagnosis and prognosis of cancers in humans and animals,
CC particularly breast, gastric and colorectal cancer; for treatment of
CC these cancers; and to screen for inhibitors of MAB. The present sequence

CC represents the monoclonal antibody of the invention.

XX Sequence 403 AA;

Query Match 58.5%; Score 1057.5; DB 8; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQPVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMNSGTPDILTRHFT 73
DB 82 TSVPHVSRPLNNTOKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKQIEKEGVHQLRREIEIQAH 133
DB 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKLVLFKAQLEKAGVHQLRREVEIQSHLR 189

QY 134 HNNILRLNYFYDRIIRYILLEYAPRGELYKELQKSCCTDEORTATIMEELADALMYCHG 193
DB 190 HNNILRLNYFYDRIIRYILLEYAPRGELYKELQKSCCTDEORTATITELANALSYCHS 249

QY 194 KKVHRIKIPENLLGLKGLKGIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVHRIKIPENLLGLKGLKGIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 309

QY 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
DB 310 QRPMLREVLEHPWITANSKK---PSNCQN 395

QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 36
ADK67720
ID ADK67720 standard; protein; 403 AA.

XX ADK67720;

DT 06-MAY-2004 (first entry)

XX Human modifier of AXIN (MAX) polypeptide.

XX Human; modifier of AXIN; MAX; cytostatic; gene therapy; protein kinase; enzyme.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 31 /note= "Encoded by TTT"

FT Misc-difference 104 /note= "Encoded by TC"

FT Misc-difference 128 /note= "Encoded by TG"

FT Misc-difference 235 /note= "Encoded by AACT"

FT Misc-difference 240 /note= "Encoded by TT"

XX WO2004013308-A2.

XX 12-FEB-2004.

XX 06-AUG-2003; 2003WO-US024560.

XX 06-AUG-2002; 2002US-0401534P.

PR 16-SEP-2002; 2002US-0411153P.

XX (EXEL-) EXELIXIS INC.

XX Gendreau SB, Dora EG, Lickteig K, Amundsen CD;

XX

DR WPI; 2004-157122/15.
DR N-PSDB; ADK67713.

XX Identifying a candidate AXIN pathway-modulating agent, useful in diagnosing and treating cancer, comprises providing an assay system comprising a MAX polypeptide or nucleic acid.

XX Example 1; SEQ ID NO 11; 74pp; English.

XX The present sequence is that of a human modifier of AXIN (MAX) polypeptide characterised as a serine/threonine kinase. Genetic screens were designed to identify modifiers of the axin pathway in Caenorhabditis elegans, where a reduction of function pry-1 (axin) mutant was used. Genes causing altered phenotypes were isolated, and their human homologues, termed MAX, were identified, including the present sequence. These MAX polynucleotides and polypeptides are attractive targets for the treatment of pathologies associated with a defective AXIN signalling pathway, such as cancer. Modulation of MAX or its binding partner is useful for understanding the association of the AXIN pathway and its members in normal and disease conditions and for developing diagnostic and therapeutic modalities for AXIN related pathologies. MAX-modulating agents that act by inhibiting or enhancing MAX expression, directly or indirectly, e.g. by affecting MAX function can be identified using methods of the invention. MAX modulating agents are useful in diagnosis, therapy and pharmaceutical development. Preferred MAX modulating agents include antisense and phosphorothioate morpholino oligomers.

XX Sequence 403 AA;

Query Match 58.5%; Score 1057.5; DB 8; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;

QY 22 STLQPVLR-----KEPVTPSALVLMRSNVQPTAAPGQKVMNSGTPDILTRHFT 73
DB 82 TSVPHVSRPLNNTOKSKQPL-PSA-----PENNPEELASKQKNESKK-----RQWA 129

QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKQIEKEGVHQLRREIEIQAH 133
DB 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKLVLFKAQLEKAGVHQLRREVEIQSHLR 189

QY 134 HNNILRLNYFYDRIIRYILLEYAPRGELYKELQKSCCTDEORTATIMEELADALMYCHG 193
DB 190 HNNILRLNYFYDRIIRYILLEYAPRGELYKELQKSCCTDEORTATITELANALSYCHS 249

QY 194 KKVHRIKIPENLLGLKGLKGIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVHRIKIPENLLGLKGLKGIADFGWSVHAPSLRRKTMCGTLDYLPPEMIEGRMHNEK 309

QY 254 VDLWCIGVLCYELLVGNPPFPESASHNETYRRIVKVDLKFPPASVPTGAQDLISKLLRHNP 313
DB 310 VDLWLSGLVLCYEFVGVKPPFEANTYQTYKISRVEFTFPDFVTEGARDLISRLKHNPS 369

QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPMLREVLEHPWITANSKK---PSNCQN 395

RESULT 37
ADM72205
ID ADM72205 standard; protein; 403 AA.

XX ADM72205;

XX 17-JUN-2004 (first entry)

XX Human TASK104 polypeptide.

XX TASK; tumour-associated kinase; cytostatic; tumour antigen; cell proliferative disorder; cancer; transgenic; human.

XX Homo sapiens.

XX

PN WO2004024064-A2.
XX 25-MAR-2004.
XX 05-SEP-2003; 2003WO-US027894.
XX 11-SEP-2002; 2002US-0410166P.
XX (GETH) GENENTECH INC.
XX Desauvage FJ, Wood WI, Zhang Z;
PI WPI; 2004-282985/26.
DR N-PSDB; ADM72204.
XX New tumor-associated kinase nucleic acids and polypeptides, useful as
PT hybridization probes for isolating full length TASK DNA, for generating
PT transgenic animals, in chromosome identification, or for tissue typing.
XX Claim 12; SEQ ID NO 10; 163pp; English.
XX The invention relates to new isolated tumour-associated kinase (TASK)
CC nucleic acid molecules and encoded polypeptides. Cytostatic. The
CC antibody, oligopeptide or organic molecule that binds to the TASK
CC polypeptide are useful for treating a mammal having a tumour comprising
CC cells expressing the polypeptide. Antagonists of TASK are useful for
CC treating or preventing a cell proliferative disorder (e.g. cancer)
CC associated with increased expression or activity of TASK polypeptide. The
CC TASK polynucleotides and polypeptides may be used as hybridization probes
CC for isolating full length TASK DNA, for generating transgenic animals, in
CC chromosome identification, or for tissue typing. The present sequence
XX represents a human TASK polypeptide.
SQ Sequence 403 AA;
Query Match 58.5%; Score 1057.5; DB 8; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLPRVLR-----KEPVTSPALVMSRSNVQPTAAPGQKWMENSGTPDILTRHFT 73
DB 82 TSPVHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----ROWA 129
QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKVLFAQLKAGVEHQLRREIEIOAHLH 189
QY 134 HFNILRLYNYFYDRRIYILLEYAPRGELYKELQKSCFTDEORTATIMBELADALMYCHG 193
DB 190 HFNILRLYGYFHDATRVYLLEYAPLGTVYVRELQKLSKFDEQRTATYITELANALSYCHS 249
QY 194 KKVIRHDIKPNELLGLKGLKIADFGWSVHAPSRLRKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVIRHDIKPNELLGLKGLKIADFGWSVHAPSRLRKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRIVKDLKFPASVPTGAQDLISKLRLHNS 313
DB 310 VDLWSGLVLCYELFLVGKPPFEANTYQETKYRISRVETFPDFVTEGARDLISKLRLHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
DB 370 QRPMLEVLHPWITANSKK---PSNCQN 395
RESULT 38
ADQ89832
ID ADQ89832 standard; protein; 403 AA.
XX ADQ89832;
XX ADQ89832;
DT 21-OCT-2004 (first entry)
XX Antagonist of cell cycle progression polypeptide #131.

XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX Homo sapiens.
XX WO2004063362-A2.
XX 29-JUL-2004.
XX 31-DEC-2003; 2003WO-GB005635.
XX 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX (CYCL-) CYCLACEL LTD.
XX Glover D, Bell G, Frenz L, Midgley C;
XX WPI; 2004-544089/52.
DR N-PSDB; ADQ89831.
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX Claim 2; SEQ ID NO 262; 461pp; English.
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX sequence.
SQ Sequence 403 AA;
Query Match 58.5%; Score 1057.5; DB 8; Length 403;
Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLPRVLR-----KEPVTSPALVMSRSNVQPTAAPGQKWMENSGTPDILTRHFT 73
DB 82 TSPVHPVSRPLNNTQSKQPL-PSA-----PENNPEELASKQNEESKK-----ROWA 129
QY 74 IDDFEIGRPLGKGFNVYLAREKSHFIVALKVLFKSOIEKEGVHQLRREIEIOAHLH 133
DB 130 LEDFEIGRPLGKGFNVYLAREKSKFIALKVLFAQLKAGVEHQLRREIEIOAHLH 189
QY 134 HFNILRLYNYFYDRRIYILLEYAPRGELYKELQKSCFTDEORTATIMBELADALMYCHG 193
DB 190 HFNILRLYGYFHDATRVYLLEYAPLGTVYVRELQKLSKFDEQRTATYITELANALSYCHS 249
QY 194 KKVIRHDIKPNELLGLKGLKIADFGWSVHAPSRLRKTCGTLDYLPPEMIEGRMHNEK 253
DB 250 KKVIRHDIKPNELLGLKGLKIADFGWSVHAPSRLRKTCGTLDYLPPEMIEGRMHNEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRIRIVKDLKFPASVPTGAQDLISKLRLHNS 313
DB 310 VDLWSGLVLCYELFLVGKPPFEANTYQETKYRISRVETFPDFVTEGARDLISKLRLHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRLVPPSALQS 342
DB 370 QRPMLEVLHPWITANSKK---PSNCQN 395
RESULT 39

ADR05174
ID ADR05174 standard; protein; 403 AA.
XX
AC ADR05174;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human GTPase regulator-associated w focal adhesion kinase pp125 protein.
XX
KW apoptosis; cytoskeletal; antiinflammatory; antiasthmatic; respiratory;
KW antihemetic; antiarthritic; gynaecological; cardiac; vasotropic;
KW antiproliferative; antitumor; gastrointestinal; immunosuppressive;
KW neuroprotective; cancer; autoimmune; neurodegenerative; inflammatory;
KW asthma; chronic obstructive pulmonary disease; cystic fibrosis;
KW rheumatoid arthritis; acute respiratory distress syndrome; preclampsia;
KW myocardial ischaemia; reperfusion injury; psoriasis; bronchiolitis;
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; human;
KW enzyme; GTPase regulator-associated with focal adhesion kinase pp125;
GPAF.
XX
OS Homo sapiens.
XX
XX WO2004085959-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-GB000271.
XX
XX 23-JAN-2003; 2003GB-00001566.
XX
XX 25-MAR-2003; 2003US-0457533P.
XX
XX (BIRX-) EIRX THERAPEUTICS LTD.
XX
XX Seery L, Hayes I, Murphy F;
XX
XX WPI; 2004-593556/57.
XX
XX N-PSDB; ADR05175.
XX
XX Identifying a modulator of apoptosis-associated polypeptide function,
XX useful for treating e.g., cancer, comprises incubating a sample
XX containing an apoptosis-associated polypeptide and a candidate agent to
XX permit binding.
XX
XX Claim 1; Page; 230pp; English.
XX
XX The invention relates to a novel method for identifying an agent that
XX modulates the function of an apoptosis-associated polypeptide,
XX particularly a kinase or GPCR (G-protein-coupled receptor). The method
XX comprises providing a sample containing an apoptosis-associated
XX polypeptide and a candidate agent and incubating under conditions to
XX permit binding of the candidate agent to the polypeptide, measuring the
XX binding and comparing it with the binding of the polypeptide to a control
XX agent known not to bind to the polypeptide. The method of the invention
XX has cytostatic, antiinflammatory, antiasthmatic, respiratory,
XX antitumor, antiarthritic, gynaecological, cardiac, vasotropic,
XX antiproliferative, antitumor, gastrointestinal, immunosuppressive and
XX neuroprotective applications. The method and molecules may be useful for
XX treating a disease or condition characterised by abnormal apoptosis in
XX mammalian tissue, particularly cancer, such as small cell lung cancer,
XX cancer of the kidney, uterus, prostate, bladder, ovary, colon and breast,
XX leukaemias, sarcomas and myelomas. Furthermore, autoimmune,
XX neurodegenerative and inflammatory conditions may be treated, including
XX asthma, chronic obstructive pulmonary disease, cystic fibrosis,
XX rheumatoid arthritis, acute respiratory distress syndrome, preclampsia,
XX myocardial ischaemia, reperfusion injury, psoriasis, bronchiolitis,
XX Crohn's disease, ulcerative colitis and inflammatory bowel disease. The
XX current sequence is that of a human apoptosis-associated protein of the
XX invention which was used during siRNA (small interfering RNA)-mediated
XX gene silencing.
XX
XX Sequence 403 AA;

Query Match

58.5%; Score 1057.5; DB 8; Length 403;

Best Local Similarity 63.2%; Pred. No. 1.3e-104;
Matches 208; Conservative 41; Mismatches 57; Indels 23; Gaps 5;
QY 22 STLPRVLR-----KEPTPSALVMSRNVQPTAAPGOKVMENSSGTPDILTRHFT 73
DB 82 TSVPHFVSRLNNTQSKQPL-PSA-----PENNPEELASKOKNEESKK-----RQWA 129
QY 74 IDDFEIGRPLGKGFNGVYLAREKSHFVALKVLFSQIEKEGVEHQLRREIEIOAHILH 133
DB 130 LEDFEIGRPLGKGFNGVYLAREKSKFIALKVLFAKLEKAGVEHQLRREVEIOSHLR 189
QY 134 HPNILRLNRYFYDRRIYILLEYAPRGELYKELQSKCTDEORTATIMELADALMYCHG 193
DB 190 HPNILRLYGFHDATRVYILEYAPLGTVYRBLQKLSKEDEQRTATYITELANALSYCHS 249
QY 194 KKVIRHDIKPENLILGKELKIALDFGWSHAPSARRKTCGTLDVLPPEMIEGRMHNEK 253
DB 250 KKVIRHDIKPENLILGKELKIALDFGWSHAPSARRKTCGTLDVLPPEMIEGRMHDEK 309
QY 254 VDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPPASVPTGAOLISKLHNPFS 313
DB 310 VDLWSLGVLCYBFLVGKPPFEANTYQETVKRISRVEFTFPDFVTEGARDLISLLAKHNS 369
QY 314 ERLPLAQVSAHPWVRANSRRVLPSPALQS 342
DB 370 QRPLREVLHPWITANSK---PSNCQN 395
RESULT 40
ABP41958
ID ABP41958 standard; protein; 420 AA.
XX
AC ABP41958;
XX
DT 22-AUG-2002 (first entry)
XX
DE Human ovarian antigen HPCOK03, SEQ ID NO:3090.
XX
XX Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX antiinflammatory; gynaecological; reproductive; chromosome 20q13.2-13.3.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US018569.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
XX
XX WPI; 2002-147878/19.
XX
XX N-PSDB; ABQ55035.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX cancer), immune disorders, cardiovascular disorders and neurological
XX diseases.
XX
XX Claim 11; SEQ ID NO 3090; 2922pp; English.
XX

CC oncogenesis - the Aurora A gene maps to chromosome 20q13, a region which
CC is frequently amplified in human tumours including breast and colon
CC tumours, and it is overexpressed in over 50% of primary colorectal
CC tumours. The crystal structure of human Aurora A kinase may be used to
CC select or design chemical modulators of Aurora kinase, particularly
CC Aurora kinase inhibitors. These modulators may be used to prevent or
CC treat undesirable physical and pharmacological consequences of
CC inappropriate Aurora activity, especially cancers or other
CC hyperproliferative disorders. The Aurora A kinase 3D structure may also
CC be used in designing an Aurora protein or Aurora homologue, and in
CC elucidating the 3D structure of other proteins with structural similarity
CC to Aurora kinases. The present sequence represents a truncated T287D
CC mutant Aurora A kinase sequence which was prepared and crystallised in an
CC example from the invention. This sequence comprises the Aurora A kinase
CC domain and also contains a vector-encoded sequence at the N-terminus
XX
SQ Sequence 319 AA;

Query Match 58.1%; Score 1050.5; DB 6; Length 319;
Best Local Similarity 65.4%; Pred. No. 5.3e-104;
Matches 204; Conservative 38; Mismatches 55; Indels 15; Gaps 4;

QY 31 KEPTVSALVMSRSNVQTAAPGCKVMENSSGTPDILTRHFTIDDFEIGRPLGKGFKN 90
DB 15 KOPL-PSA-----PENNPEELASQKNESKK-----RQWALEDFEIGRPLGKGFKN 62
QY 91 VYLAREKSHFIVALKVLPKSOIEKEGVEHQLRRETEIOAHLHPNLRILNYFYDRRI 150
DB 63 VYLAREKQSFIALKVLFAQLEKAGVEHQLRREVEIOSHLRHPNLRILNYFYFHDTRV 122
QY 151 YLILEYAPRGELYKELQKSTFDEQRTATIMEADALMYCHGKVIHRDIKPENLLGL 210
DB 123 YLILEYAPLGTVYRELQKSKFDEQRTATITELANALSYCHSKRVHRDIKPENLLGS 182
QY 211 KGLKIADFQSWHAPSLRRKTCGTLDYLPPEMIEGRMHNEKVDLWCIGVLCYELLVGN 270
DB 183 AGELKIADFQSWHAPSSRRTDLCGTLDYLPPEMIEGRMHNEKVDLWSLGVLCYELVGK 242
QY 271 PPESASHNETYRRIKVDLPKPSVPTGAODLISKLHNPSERLPLAQVSAHPWVRAN 330
DB 243 PPEANTYQTYKRIKRVETFPDFVTEGARDLISRLKHNPQSQRPMLEHHPWITAN 302
QY 331 SREVLPPSALQS 342
DB 303 SSK---PSNCQN 311

RESULT 42
ADJ31727
ID ADJ31727 standard; protein; 403 AA.
XX
AC ADJ31727;
XX
DT 22-APR-2004 (first entry)
XX
DE Human mitotic kinase hARK.
XX
KW Human; enzyme; SAK; Snk Akin Kinase; serine/threonine protein kinase;
KW mitotic kinase; cellular proliferation; chemosensitivity; cancer;
KW proliferative disorder; cytostatic; hARK.
XX
OS Homo sapiens.
XX
PN US2003027756-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00026021.
XX
PR 01-AUG-2001; 2001US-0309632P.
XX
PA (RIGB-) RIGEL PHARM INC.
XX

PI Hitoshi Y, Demo S, Jenkins Y;
XX WPI; 2003-479546/45.
XX
XX Modulating cellular proliferation in subject, by administering
PT serine/threonine protein kinase involved in modulation of cellular
PT proliferation and cell cycle regulation, or a nucleic acid encoding the
PT polypeptide.
XX
XX Example 1; Fig 2; 41pp; English.
XX
CC The invention relates to modulating (M1) cellular proliferation in a
CC subject, involves administering to the subject a serine/threonine protein
CC kinase involved in modulation of cellular proliferation and cell cycle
CC regulation (SAK polypeptide, Snk Akin Kinase, a mitotic kinase) encoded
CC by a nucleic acid that hybridises under stringent conditions to a nucleic
CC acid encoding a polypeptide appearing as ADJ31723. Also included are
CC identifying (M2) a compound capable of interfering with binding of SAK or
CC its fragment (by combining SAK or its fragment with Chk2 polypeptide and
CC the compound, where SAK or its fragment has kinase activity, and
CC determining the binding of SAK or its fragment to Chk2), identifying (M3)
CC a compound that modulates cellular proliferation (by contacting the
CC compound with SAK, and determining the functional effect of the compound
CC on SAK), identifying (M4) a compound that modulates cellular
CC proliferation or chemosensitivity, (by contacting the compound with SAK
CC or its fragment, and determining the physical effect of the compound on
CC SAK), determining the chemical or phenotypic effect of the compound upon
CC a cell comprising SAK or its fragment and modulating (M5) cellular
CC proliferation in a subject (by administering to the subject a compound
CC identified by M3). M1 or M5 is useful for modulating cellular
CC proliferation in a subject, preferably a human having cancer. M2 is
CC useful for identifying a compound capable of interfering with binding of
CC SAK or its fragment. M3 is useful for identifying a compound that
CC modulates cellular proliferation. M4 is useful for identifying a compound
CC that modulates cellular proliferation or chemosensitivity, where the
CC compound is an antibody, antisense molecule, small organic molecule, or
CC circular peptide. M1 or M5 or the compound identified by M3 or M4 is
CC useful for treating cancer and other proliferative disorders. The present
CC sequence represents a human mitotic kinase similar to SAK.
XX
SQ Sequence 403 AA;

Query Match 58.1%; Score 1050.5; DB 7; Length 403;
Best Local Similarity 61.7%; Pred. No. 7.6e-104;
Matches 209; Conservative 40; Mismatches 67; Indels 23; Gaps 5;

QY 4 KENSYPWPYGRQTAPSGSLSTLPQVLRKEPVTPTPSALVMSRSNVQTAAPGCKVMENSSG 63
DB 80 QQTSVPHPVSR-----PLNNTQSKOPL-PSA-----PENNPEELASQKNESKK- 125
QY 64 TPDILTRHFTIDDFEIGRPLGKGFKNVYLAREKSHFIVALKVLPKSOIEKEGVEHQLR 123
DB 126 -----RQWALEDFEIGRPLGKGFKNVYLAREKSHFIVALKVLPKAGVEHQLR 179
QY 124 REIEIOAHLHPNLRILNYFYDRRIYLIILEYAPRGELYKELQKSTFDEQRTATIMEE 183
DB 180 REVEIQSHLRHPNLRILNYFYFHDTRVYLIILEYAPLGTVYRELQKSKFDEQRTATYTE 239
QY 184 LADALMYCHGKVIHRDIKPENLLGLKELKIADFQSWHAPSLRRKTCGTLDYLPPE 243
DB 240 LANALSYCHSKRVHRDIKPENLLGLSAGELKIADFQSWHAPSSRRTTLCGTLDYLPPE 299
QY 244 MTEGRMHNEKVDLWCIGVLCYELLGNPPESASHNETYRRIKVDLPKPSVPTGAODL 303
DB 300 MTEGRMHNEKVDLWSLGVLCYELFKVGPPEANTYQTYKRIKRVETFPDFVTEGARDL 359
QY 304 ISKLHNPSERLPLAQVSAHPWVRANRRVLPSPALQS 342
DB 360 ISRLKHNPQSQRPMLEHHPWITANSSK---PSNCQN 395

RESULT 43
ABR61579

FT	Domain	124. -283	/label= C-terminal domain	/note= "Corresponds to residues 215-374 of the native human Aurora A kinase"	Misc-difference 196	/note= "Asp replaces wild-type Thr. Corresponds to position 287 of the native human Aurora A kinase"
XX	WO2003031606-A2.					
XX	17-APR-2003.					
XX	08-OCT-2002; 2002WO-GB004589.					
XX	10-OCT-2001; 2001GB-00024299.					
XX	(ASTR) ASTRAZENECA AB.					
XX	(ASTR) ASTRAZENECA UK LTD.					
XX	Anderson M, Keen NJ, Pannifer ADB, Paupit RA, Rowsell S;					
XX	WPI; 2003-403104/38.					
XX	Novel crystalline form of polypeptide comprising catalytic domain of Aurora kinase, whose atomic coordinate data is useful for designing or selecting Aurora chemical inhibitor, and for designing an Aurora protein.					
XX	Example 1; Page 119; 137pp; English.					
XX	The invention relates to the three-dimensional structure of human Aurora A kinase. The invention describes the methods used to prepare and crystallise truncated mutant forms of human Aurora A kinase comprising the catalytic domain, which were then subjected to X-ray crystallography to generate atomic coordinates. The mutant forms of Aurora A used in the invention all contain a T287D substitution, which produces a mimic of activated protein which can be provided as a homogeneous sample (native Aurora A kinase is activated by phosphorylation of T287). Two crystalline forms of the Aurora A kinase catalytic domain were produced - one complexed with the hydrolysable ATP analogue ANP-PNP, and one complexed with a synthetic inhibitor. The ATP analogue was found to occupy a cleft between the N-terminal domain (residues 125-208) and the C-terminal domain (residues 215-374). Aurora A kinase is a serine/threonine kinase which is involved in cell cycle regulation, with its expression and activity peaking at the G2/M boundary. It has been implicated in oncogenesis - the Aurora A gene maps to chromosome 20q13, a region which is frequently amplified in human tumours including breast and colon tumours, and it is overexpressed in over 50% of primary colorectal tumours. The crystal structure of human Aurora A kinase may be used to select or design chemical modulators of Aurora kinase, particularly Aurora kinase inhibitors. These modulators may be used to prevent or treat undesirable physical and pharmacological consequences of inappropriate Aurora activity, especially cancers or other hyperproliferative disorders. The Aurora A kinase 3D structure may also be used in designing an Aurora protein or Aurora homologue, and in elucidating the 3D structure of other proteins with structural similarity to Aurora kinases. The present sequence represents a truncated T287D mutant Aurora A kinase sequence which was prepared and crystallised in an example from the invention. This sequence comprises the Aurora A kinase domain and also contains a vector-encoded sequence at the N-terminus					
XX	Sequence 309 AA;					
XX	Query Match	57.7%;	Score 1043.5;	DB 6;	Length 309;	
XX	Best Local Similarity	67.5%;	Pred. No. 2.9e-103;			
XX	Matches 195;	Conservative 37;	Mismatches 54;	Indels 3;	Gaps 1;	
Qy	54 GQKVMSSGTPDILTRHFTIDDFEIGRPLGKGFNVLAREKSHFIVALKVLFKSI	113				
Db	18 GSHMLAKQKNEESKQWALEDFEIGRPLGKGFNVLAREKSKFIALKVLKFAQL	77				
Qy	114 EKEGVHQURRIEIQALHHPHNIILRLNYFDRIIRVILLEYAPRGELYKELQKCTFD	173				
Db	78 EKAGVHQURREVEIQSHLRHNIILRLNYFDRIIRVILLEYAPRGELYKELQKCTFD	137				


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AC AAO18740;
XX
XX 24-OCT-2002 (first entry)
XX
XX Human NOV4 protein.
DE
XX Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;
XX storage disorder; muscle disorder; neurodegenerative disorder; nontropic;
XX developmental defect; neuroprotective; antiparkinsonian; hypotensive;
XX hypertensive; haemostatic; cardiant; antiangiogenic; dermatological.
XX immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;
XX antiparasitic; antiallergic; antiaesthetic; antirheumatic; antiarthritic;
XX vulnery; anorectic; antidiabetic; immunomodulator; antipsoriatic;
XX nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;
XX antiinfertility; antinamic; antidepressant; metabolic; cytostatic;
XX tranquilizer; analgesic.
XX
XX Homo sapiens.
XX
XX WO200257450-A2.
XX
XX 25-JUL-2002.
XX
XX 29-NOV-2001; 2001WO-US048922.
XX
XX 29-NOV-2000; 2000US-0253834P.
XX
XX 30-NOV-2000; 2000US-0250926P.
XX
XX 25-JAN-2001; 2001US-0264180P.
XX
XX 20-AUG-2001; 2001US-0313656P.
XX
XX 05-OCT-2001; 2001US-0327456P.
XX
XX 28-NOV-2001; 2001US-00327456.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Edinger S, Macdougall JR, Millet I, Ellerman K, Stone DJ;
XX Gerlach V, Grosse WM, Alsobrook JP, Lepley DM, Rieger D, Burgess CS;
XX Casman SJ, Spytek KA, Boldog FL, Li L, Padigaru M, Mishra V;
XX Patturajan M, Shenoy S, Rastelli L, Tchernev VT, Vernet CAM;
XX Zerhusen BD, Malyankar UM, Guo X, Miller CE, Gangolli EA;
XX
XX WPI; 2002-590741/63.
XX
XX N-PSDB; ABT06285.
XX
XX Novel isolated polypeptide, designated NOVX, useful for treating or
XX preventing in NOVX-associated disorders e.g. cardiomyopathy,
XX atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.
XX
XX Claim 1; Page 62; 353pp; English.
XX
XX The present invention provides the protein and coding sequences of
XX several novel human proteins, designated NOVX. These can be used in the
XX treatment of, amongst others, cancers, autoimmune diseases, infections,
XX inflammatory diseases, storage disorders, muscle disorders,
XX neurodegenerative diseases and developmental defects. The present
XX sequence is a protein of the invention
XX
XX Sequence 403 AA;
XX
XX Query Match 53.4%; Score 966; DB 5; Length 403;
XX Best Local Similarity 61.8%; Pred. No. 9.9e-95;
XX Matches 186; Conservative 41; Mismatches 68; Indels 6; Gaps 2;
XX
XX 45 SNVQPTAAP--GQKWNSSGTPDILTRHTTDDFEIGRPLGKFGNVYLAREKKSHF 101
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 98 SKQSPUSAPENNPEELASQKNEESKQWALEDEIGRPQKGFQNVYLAREKQSKF 157
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 102 IVALKVLFSQIBKEGVEHQLRREIEIQALHHPNIRLYNYFYDRRRYLIILEYAPRGE 161
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 158 ILALRVLFKAQLEKAGVEHQLRREVEIQSHQHPNIRLYGYFHDATRVYLIILEYPLET 217
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 162 LYELOKSCTFDQRTATIMEELADALMYCHGKVIVHRDKPENLLGLGKELKIADFGW 221
XX ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 218 VNTELOKSLKSFDEORTATYITELASALSYCHSKTVIHRDIKPNENLLIGSAGELEIANFGW 277
XX
XX 222 SVHAPSLRRKTCMTGLDYLPPEMIEGRMNEKVDLMICIGVLCYELVGNPPFESASHNET 281
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 278 SEHAPSSRRTTLCGTLDYLPPEMIEGRMDEKVDLSLGLVLCCEFLVGVKPFPEANTYQET 337
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 282 YRIRVKDLKFPASVPTGAODLISKLLRNPSERLPLAQSAPHPWTRNSRRVLPFSAQ 341
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 338 YKRISRVEFTFDFVTEGARDLISRLKHVPSQRPMLREVLYBYPWITANSSK---PSNCQ 394
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 342 S 342
XX :
XX 395 N 395
XX
XX RESULT 48
XX ADJ49242
XX ID ADJ49242 standard; protein; 294 AA.
XX
XX AC ADJ49242;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Oil-associated gene related protein #742.
XX
XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
XX OS Unidentified.
XX
XX FN US2004025202-A1.
XX
XX PD 05-FEB-2004.
XX
XX PF 14-MAR-2003; 2003US-00389566.
XX
XX PR 15-MAR-2002; 2002US-0365301P.
XX
XX PR 26-JUN-2002; 2002US-0391786P.
XX
XX PR 26-JUN-2002; 2002US-0392018P.
XX
XX (LAUR/) LAURIE C C.
XX (RAVA/) RAVANELLO M.
XX (SAVA/) SAVAGE T.
XX (LEDE/) LEDEAUX J R.
XX (ROGE/) ROGERS J A.
XX
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
XX WPI; 2004-142693/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX
XX Example 3; SEQ ID NO 1246; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents the amino acid
XX sequence of an oil-associated gene related protein.
XX
XX Sequence 294 AA;
XX
XX Query Match 52.0%; Score 940; DB 8; Length 294;
XX Best Local Similarity 60.3%; Pred. No. 3.9e-92;
XX Matches 179; Conservative 47; Mismatches 63; Indels 8; Gaps 4;
XX
XX 49 PTAAPQKWNSSGTPDILTRHTTDDFEIGRPLGKFGNVYLAREKKSHFIVALKVL 108
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
XX 4 PTEQHOE-KEASDASAAAAQKRWTLSDFDIGKPLGRKFGHVYLAREKRNHVVALKVL 62
XX |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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QY 109 FKSQIEKEGVEHOLRRREIBIQAHLHPNIIIRLNYFYDVRRIYILLYAARGELYKELOK 168
 DB 63 FKSQLOOQSQVEHQRRREVEIQSHLRHPNIIIRLNYFYDQKRVYILLYAARGELYKLOK 122
 QY 169 SCTFDEORTATIMEELADALMYCHGKVIHRDIKPNILLLGKELKIADFGSVHAPSL 228
 DB 123 CKYFSERRATYVASLARALIYCHGKVIHRDIKPNILLLGKELKIADFGSVHFTFN- 181
 QY 229 RRKTMCGTLDYLPPEMIEGRMHNEKVDLCIGVLCYELLVGNPPFESASHNETYRIRVKV 288
 DB 182 RRKTMCGTLDYLPPEMVESVEHDASVDIWSLGIILCYEFLYGVPPFEAMEHSDIYRIRVQV 241
 QY 289 DLKFPAS--VPTGAQDLISKLRHNPSEIRPLAQVSAHPWVRANSRRLVPPSALQSV 343
 DB 242 DLKFPKPIISASAKDLISQMLVKSSORLPLHKLHPWVQNA----DPSGIYRV 294

RESULT 49
 ADJ49602
 ID ADJ49602 standard; protein; 294 AA.
 XX AC ADJ49602;
 XX AC
 XX DT 06-MAY-2004 (first entry)
 XX DE
 XX OS Oil-associated gene related protein #1102.
 XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX OS Unidentified.
 XX PN US2004025202-A1.
 XX PD 05-FEB-2004.
 XX PF 14-MAR-2003; 2003US-00389566.
 XX PR 15-MAR-2002; 2002US-0365301P.
 XX PR 26-JUN-2002; 2002US-0391786P.
 XX PR 26-JUN-2002; 2002US-0392018P.
 XX PA (LAUR/) LAURIE C C.
 XX PA (RAVA/) RAVANELLO M.
 XX PA (SAVA/) SAVAGE T.
 XX PA (LEDE/) LEDEAUX J R.
 XX PA (ROGE/) ROGERS J A.
 XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 XX DR WPI; 2004-142683/14.
 XX PT Novel recombinant DNA construct comprising a promoter functional in
 XX PT plants operably linked to an oil-associated gene for producing transgenic
 XX PT plant seed.
 XX PS Example 3; SEQ ID NO 1606; 22pp; English.
 XX PS The invention relates to a recombinant DNA construct comprising a
 XX CC promoter functional in plants operably linked to an oil-associated gene.
 XX CC The construct is useful for transgenic plant seed which has in its genome
 XX CC the construct, that is functional in the plant to transcribe the oil-
 XX CC associated gene. The transgenic plant seed grows into a plant having
 XX CC enhanced seed oil as compared to wild type. The construct is useful for
 XX CC producing hybrid maize seed. The transgenic plant seed is useful for
 XX CC producing vegetable oil. The present sequence represents the amino acid
 XX CC sequence of an oil-associated gene related protein.
 XX SQ Sequence 294 AA;

Query Match 51.8%; Score 937; DB 8; Length 294;
 Best Local Similarity 60.3%; Pred. NO. 8.1e-92;
 Matches 179; Conservative 46; Mismatches 64; Indels 8; Gaps 4;

QY 49 PTAAPQOKVMENSSGTPDILTRHFTDDFEIGRPLGKGFENVYLAREKSHFTVALKVL 108
 DB 4 PTETQHQE-KEASDASAAAQKRWTLSDFDIGKPLGRGKFGHVYLAREKSHVVALKVL 62
 QY 109 FKSQIEKEGVEHOLRRREIBIQAHLHPNIIIRLNYFYDVRRIYILLYAARGELYKELOK 168
 DB 63 FKSQLOOQSQVEHQRRREVEIQSHLRHPNIIIRLNYFYDQKRVYILLYAARGELYKLOK 122
 QY 169 SCTFDEORTATIMEELADALMYCHGKVIHRDIKPNILLLGKELKIADFGSVHAPSL 228
 DB 123 CKYFSERRATYVASLARALIYCHGKVIHRDIKPNILLLGKELKIADFGSVHFTFN 182
 QY 229 RRKTMCGTLDYLPPEMIEGRMHNEKVDLCIGVLCYELLVGNPPFESASHNETYRIRVKV 288
 DB 183 RR-TMCGTLDYLPPEMVESVEHDASVDIWSLGIILCYEFLYGVPPFEAMEHSDIYRIRVQV 241
 QY 289 DLKFPAS--VPTGAQDLISKLRHNPSEIRPLAQVSAHPWVRANSRRLVPPSALQSV 343
 DB 242 DLKFPKPIISASAKDLISQMLVKSSORLPLHKLHPWVQNA----DPSGIYRV 294

RESULT 50
 ADJ48641
 ID ADJ48641 standard; protein; 295 AA.
 XX AC ADJ48641;
 XX DT 06-MAY-2004 (first entry)
 XX DE Oil-associated gene related protein #141.
 XX OS oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX OS Unidentified.
 XX PN US2004025202-A1.
 XX PD 05-FEB-2004.
 XX PF 14-MAR-2003; 2003US-00389566.
 XX PR 15-MAR-2002; 2002US-0365301P.
 XX PR 26-JUN-2002; 2002US-0391786P.
 XX PR 26-JUN-2002; 2002US-0392018P.
 XX PA (LAUR/) LAURIE C C.
 XX PA (RAVA/) RAVANELLO M.
 XX PA (SAVA/) SAVAGE T.
 XX PA (LEDE/) LEDEAUX J R.
 XX PA (ROGE/) ROGERS J A.
 XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 XX DR WPI; 2004-142683/14.
 XX PT Novel recombinant DNA construct comprising a promoter functional in
 XX PT plants operably linked to an oil-associated gene for producing transgenic
 XX PT plant seed.
 XX PS Example 3; SEQ ID NO 645; 22pp; English.
 XX PS The invention relates to a recombinant DNA construct comprising a
 XX CC promoter functional in plants operably linked to an oil-associated gene.
 XX CC The construct is useful for transgenic plant seed which has in its genome
 XX CC the construct, that is functional in the plant to transcribe the oil-
 XX CC associated gene. The transgenic plant seed grows into a plant having
 XX CC enhanced seed oil as compared to wild type. The construct is useful for
 XX CC producing hybrid maize seed. The transgenic plant seed is useful for
 XX CC producing vegetable oil. The present sequence represents the amino acid
 XX CC sequence of an oil-associated gene related protein.
 XX SQ Sequence 295 AA;

Query Match 51.7%; Score 934.5; DB 8; Length 295;
Best Local Similarity 65.5%; Pred. No. 1.5e-91;
Matches 173; Conservative 44; Mismatches 44; Indels 3; Gaps 2;

QY 70 RHFTTDDFIQRLPGKGFNGVYLAREKKSHFIVALKVLFKSQIEKEGVEHOLRREIEIQ 129
DB 25 RRTWLNDFDQKPLGRGFGHVLAREKTSNHIVALKVLFKSQLOQSQVHVHQLRREVEIQ 84

QY 130 AHLHHPNLRNLNYFYDRRRIYLLIYAPRGELYKELQKSCFDEORTATIMEELADALM 189
DB 85 SHLRPHILRLYGYFYDQKRVYLLIYAPKGELYKELQCKYFSERRAATYVASLARALI 144

QY 190 YCHGKXVHHRDIKPNLLIAGQELKIADFGWSVHTFN--RRRTMCGTLDLPLPPEMIEGRM 249
DB 145 YCHGKXVHHRDIKPNLLIAGQELKIADFGWSVHTFN--RRRTMCGTLDLPLPPEMIEGRM 203

QY 250 HNEKVDLCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPAS--VPTGAQDLISKL 307
DB 204 HDASVDIWSLGVLCYEFYGVPPFEAKESDTRRIIQVDLKPFPKPIVSSAAKOLISQM 263

QY 308 LRHNPSERLPLAQVSAHPWVRANS 331
DB 264 LVKDSSQRLPLHLKLEHPWIVQNA 287

RESULT 51
ADJ48640
ID ADJ48640 standard; protein; 298 AA.
XX AC ADJ48640;
XX DT 06-MAY-2004 (first entry)
XX DE Oil-associated gene related protein #140.
XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX OS Unidentified.
XX PN US2004025202-A1.
XX PD 05-FEB-2004.
XX PF 14-MAR-2003; 2003US-00389566.
XX PR 15-MAR-2002; 2002US-0365301P.
XX PR 26-JUN-2002; 2002US-0391786P.
XX PR 26-JUN-2002; 2002US-0392018P.
XX PA (LAUR/) LAURIE C C.
XX PA (RAVA/) RAVANELLO M.
XX PA (SAVA/) SAVAGE T.
XX PA (LEDE/) LEDEAUX J R.
XX PA (ROGE/) ROGERS J A.
XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX Example 3; SEQ ID NO 644; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for

CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX SQ Sequence 298 AA;

Query Match 51.6%; Score 933.5; DB 8; Length 298;
Best Local Similarity 65.5%; Pred. No. 2e-91;
Matches 173; Conservative 44; Mismatches 44; Indels 3; Gaps 2;

QY 70 RHFTTDDFIQRLPGKGFNGVYLAREKKSHFIVALKVLFKSQIEKEGVEHOLRREIEIQ 129
DB 28 RRTWLNDFDQKPLGRGFGHVLAREKTSNHIVALKVLFKSQLOQSQVHVHQLRREVEIQ 87

QY 130 AHLHHPNLRNLNYFYDRRRIYLLIYAPRGELYKELQKSCFDEORTATIMEELADALM 189
DB 88 SHLRPHILRLYGYFYDQKRVYLLIYAPKGELYKELQCKYFSERRAATYVASLARALI 147

QY 190 YCHGKXVHHRDIKPNLLIAGQELKIADFGWSVHTFN--RRRTMCGTLDLPLPPEMIEGRM 249
DB 148 YCHGKXVHHRDIKPNLLIAGQELKIADFGWSVHTFN--RRRTMCGTLDLPLPPEMIEGRM 206

QY 250 HNEKVDLCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKPAS--VPTGAQDLISKL 307
DB 207 HDASVDIWSLGVLCYEFYGVPPFEAKESDTRRIIQVDLKPFPKPIVSSAAKOLISQM 266

QY 308 LRHNPSERLPLAQVSAHPWVRANS 331
DB 267 LVKDSSQRLPLHLKLEHPWIVQNA 290

RESULT 52
ADJ49236
ID ADJ49236 standard; protein; 282 AA.
XX AC ADJ49236;
XX DT 06-MAY-2004 (first entry)
XX DE Oil-associated gene related protein #736.
XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX OS Unidentified.
XX PN US2004025202-A1.
XX PD 05-FEB-2004.
XX PF 14-MAR-2003; 2003US-00389566.
XX PR 15-MAR-2002; 2002US-0365301P.
XX PR 26-JUN-2002; 2002US-0391786P.
XX PR 26-JUN-2002; 2002US-0392018P.
XX PA (LAUR/) LAURIE C C.
XX PA (RAVA/) RAVANELLO M.
XX PA (SAVA/) SAVAGE T.
XX PA (LEDE/) LEDEAUX J R.
XX PA (ROGE/) ROGERS J A.
XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX Example 3; SEQ ID NO 1240; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC producing hybrid maize seed. The transgenic plant seed is useful for

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